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(54) Title: **COMPLETE NUCLEOTIDE SEQUENCE OF STAPHYLOCOCCUS AUREUS RIBOSOMAL PROTEIN GENE, S20 AND METHODS FOR THE IDENTIFICATION OF ANTIBACTERIAL SUBSTANCES**

(57) Abstract: **The invention provides an isolated *S. aureus* ribosomal polypeptide S20, and the isolated polynucleotide molecules that encode them, vectors and host cells comprising such polynucleotide molecules and also methods for the identification of agents that effect ribosomal assembly.**

**WO 02/08265 A2**

**Complete Nucleotide Sequence of *Staphylococcus aureus* Ribosomal Protein Gene, S20 and Methods for the Identification of Antibacterial Substances**

**CROSS REFERENCE TO RELATED APPLICATIONS**

5           The present application claims priority of Application Serial Number 60/219361 filed 19 July 2000 which is hereby incorporated by reference.

**FIELD OF THE INVENTION**

          The present invention provides an isolated *S. aureus* S20 ribosomal polypeptide, and the isolated polynucleotide molecules that encode them, as well as  
10       vectors and host cells comprising such polynucleotide molecules. The invention also provides methods for the identification of agents that effect ribosomal assembly.

**BACKGROUND**

          The staphylococci, of which *Staphylococcus aureus* is the most important human pathogen, are hardy, gram-positive bacteria that colonize the skin of most  
15       humans. Staphylococcal strains that produce coagulase are designated *S. aureus* other clinically important coagulase-negative staphylococci are *S. epidermidis* and *S. saprophyticus*. When the skin or mucous membrane barriers are disrupted, staphylococci can cause localized and superficial infections that are commonly harmless and self-limiting. However, when staphylococci invade the lymphatics and  
20       the blood, potentially serious complications may result, such as bacteremia, septic shock, and serous metastatic infections, including endocarditis, arthritis, osteomyelitis, pneumonia and abscesses in virtually any organ. Certain strains of *S. aureus* produce toxins that cause skin rashes, food poisoning, or multisystem dysfunction (as in toxic shock syndrome). *S. aureus* and *S. epidermidis* together have  
25       become the most common cause of nonsocomial non-urinary tract infection in U.S. hospitals. They are the most frequently isolated pathogens in both primary and secondary bacteremias and in cutaneous and surgical wound infections. See generally *Harrison's Principles of Internal Medicine*, 13<sup>th</sup> ed., Isselbacher et. al. eds. McGraw-Hill, New York (1994), particularly pages 611-617.

30       Transient colonization of the nose by *S. aureus* is seen in 70-90 percent of people, of which 20 to 30 percent carry the bacteria for relatively prolonged periods of time. Independent colonization of the perineal area occurs in 5-20 percent of people. Higher carriage rates of *S. aureus* have been documented in persons with atopic

dermatitis, hospital employees, hospitalized patients, patients whose care requires frequent puncture of the skin, and intravenous drug abusers.

Infection by staphylococci usually results from a combination of bacterial virulence factors and a diminution in host defenses. Important microbial factors include the ability of the staphylococcus to survive under harsh conditions, its cell wall constituents, the production of enzymes and toxins that promote tissue invasion, its capacity to persist intracellularly in certain phagocytes, and its potential to acquire resistance to antimicrobials. Important host factors include an intact mucocutaneous barrier, and adequate number of functional neutrophils, and removal of foreign bodies or dead tissue.

Once the skin or mucosa have been breached, local bacterial multiplication is accompanied by inflammation, neutrophil accumulation, tissue necrosis, thrombosis and fibrin deposition at the site of infection. Later, fibroblasts create a relatively avascular wall about the area. When host mechanisms fail to contain the cutaneous or submucosal infection, staphylococci may enter the lymphatics and the bloodstream. Common sites of metastatic spread include the lungs, kidneys, cardiac valves, myocardium, liver, spleen, bone and brain.

Antimicrobial resistance by staphylococci favors their persistence in the hospital environment. Over 90 percent of both hospital and community strains of *S. aureus* causing infection are resistant to penicillin. This resistance is due to the production of  $\beta$  lactamase enzymes. The genes for these enzymes are usually carried by plasmids. Infections due to organisms with such acquired resistance can sometimes be treated with  $\beta$  lactamase resistant penicillin derivatives. However the true penicillinase-resistant *S. aureus* organisms, called methicillin resistant *S. aureus* (MRSA), are resistant to all the  $\beta$  lactam antibiotics and the cephalosporins. MRSA resistance is chromosomally mediated and involves production of an altered penicillin-binding protein (PBP 2a or PBP 2') with a low binding for  $\beta$  lactams. MRSA frequently also have acquired plasmids mediating resistance to erythromycin, tetracycline, chloramphenicol, clindamycin, and aminoglycosides. MRSA have become increasingly common worldwide, particularly in tertiary-care referral hospitals. In the United States, approximately 32 percent of hospital isolates of *S. aureus* are methicillin resistant. Methicillin resistant staphylococci are a serious clinical and economic problem, since treatment of these infections often requires

vancomycin, an antibiotic that is more difficult to administer and more expensive than the penicillins. Quinolone antimicrobial agents have been used to treat methicillin-resistant staphylococcal infections. Unfortunately, resistance to these antibiotics has also developed rapidly. Sixty to 70% of methicillin resistant *S. aureus* isolates are also quinolone resistant.

A pressing need exists for new chemical entities that are effective in the treatment of staphylococcal infections. One fruitful area of research has been in the area of agents which inhibit protein synthesis. A large number of antibacterial agents, including many in current clinical use, inhibit protein synthesis in bacteria by interfering with essential functions of the ribosome. When ribosomal function is perturbed, protein synthesis may cease entirely or, alternatively, it may be sufficiently slowed so as to stop normal cell growth and metabolism. Differences between the prokaryotic 70S ribosomes (composed of 50S and 30S subunits) and the eukaryotic 80S ribosome (composed of 60S and 40S subunits) underlie the basis for the selective toxicity of many antimicrobial agents of this class. However, a limited subset of this class of antimicrobial agents exhibits some cross-reactivity with the 70S ribosomes of eukaryotic mitochondria. This cross-reactivity probably accounts for the host cells cytotoxicity effects observed with some agents and has limited their use as clinical antimicrobial agents. Other agents (e.g., tetracycline), which affect the function of eukaryotic 80S ribosomes in vitro, are still used clinically to treat bacterial infections as the concentrations employed during antimicrobial therapy are not sufficient to elicit host cell toxicity side-effects.

Moreover, protein biosynthesis inhibitors can be divided into a number of different classes based on differences in their mechanisms of action. The aminoglycoside agents (e.g., streptomycin) bind irreversibly to the 30S subunit of the ribosome, thereby slowing protein synthesis and causing mis-translation (i.e., mis-reading) of the mRNA. The resulting errors in the fidelity of protein synthesis are bacteriocidal, and the selective toxicity of this family of agents is increased by the fact that bacteria actively transport them into the cell. The tetracycline family of agents (e.g., doxycycline) also binds to the 30S ribosome subunit, but does so reversibly. Such agents are bacteriostatic and act by interfering with the elongation phase of protein synthesis by inhibiting the transfer of the amino acid moieties of the aminoacyl-tRNA substrates into the

growing polypeptide chain. However, inhibition mediated by the tetracyclines is readily reversible, with protein synthesis resuming once intracellular levels of the agent's decline. Chloramphenicol and the macrolide family of agents (e.g., erythromycin), in contrast, act on the function/activity of the 50S subunit of the ribosome. These agents are bacteriostatic in nature, and their effects are reversible. It has also been suggested that both chloramphenicol and the macrolides may have a second mode of action involved in ribosomal assembly. Champney and Burdine (1995). Finally, puromycin acts as a competitive inhibitor of the binding of aminoacyl-tRNA's to the so-called aminoacyl site (i.e., A-site) of the ribosome and acts as a chain-terminator of the elongation phase as a result of its incorporation into the growing peptide chain.

It has been shown in *E. coli* that mutants which lack S20 in ribosomes, as judged by 2-dimensional electrophoresis are impaired in 30S subunit association with 50S subunits to form 70S ribosomes. Ryden-Aulin et al. (1993) Molecular Microbiology 7(6) 983-992. The mutants described by Ryden-Aulin misread nonsense codons and show a greatly reduced growth rate. Because of this growth impairment S20 ribosomal polypeptide is an attractive molecular target for the development of antibacterial agents effective against *S. aureus* and related organisms. It has also been noted that mitochondrial ribosomes lack a homolog of the bacterial S20 protein. Koc et al. (2001) J. Biol. Chem 276 (22) 19363-19374. The lack of a mitochondrial counterpart makes S20 even more attractive as a bacteria-specific target.

This document discloses important new methods of identifying antibacterial substances related to the bacterial ribosomal assembly process, and to the *Staphylococcal* ribosomal protein S20 and it for the first time discloses the full nucleotide and amino acid sequence of *Staphylococcus aureus* S20 ribosomal polypeptide

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#### 20 **Brief Description of the Sequence Listings**

- SEQ ID NO:1 Complete coding sequence of S20 ribosomal polypeptide
- SEQ ID NO:2 Predicted polypeptide sequence of S20 ribosomal polypeptide
- SEQ ID NO:3 Sequencing Primer
- SEQ ID NO:4 Sequencing Primer
- 25 SEQ ID NO:5 Sequencing Primer
- SEQ ID NO:6 Sequencing Primer
- SEQ ID NO:7 Sequencing Primer
- SEQ ID NO:8 Sequencing Primer
- SEQ ID NO:9 PCR Primer
- 30 SEQ ID NO:10 PCR Primer
- SEQ ID NO:11 DNA sequence for *Staphylococcus aureus* S4 ribosomal protein gene (coding and flanking sequences)
- SEQ ID NO:12 Polypeptide sequence for *Staphylococcus aureus* S4 ribosomal protein
- SEQ ID NO:13 DNA sequence for *Staphylococcus aureus* S7 ribosomal protein gene
- 35 (coding and flanking sequences)
- SEQ ID NO:14 Polypeptide sequence for *Staphylococcus aureus* S7 ribosomal protein
- SEQ ID NO:15 DNA sequence for *Staphylococcus aureus* S8 ribosomal protein gene (coding and flanking sequences)
- SEQ ID NO:16 Polypeptide sequence for *Staphylococcus aureus* S8 ribosomal protein



- SEQ ID NO:17 DNA sequence for *Staphylococcus aureus* S15 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:18 Polypeptide sequence for *Staphylococcus aureus* S15 ribosomal  
protein
- 5 SEQ ID NO:19 DNA sequence for *Staphylococcus aureus* S17 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:20 Polypeptide sequence for *Staphylococcus aureus* S17 ribosomal  
protein
- 10 SEQ ID NO:21 DNA sequence for *Staphylococcus aureus* 16S ribosomal RNA gene  
(coding and flanking sequences)
- SEQ ID NO:22 DNA sequence for *Staphylococcus aureus* S1 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:23 Polypeptide sequence for *Staphylococcus aureus* S1 ribosomal protein  
gene
- 15 SEQ ID NO:24 DNA sequence for *Staphylococcus aureus* S2 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:25 Polypeptide sequence for *Staphylococcus aureus* S2 ribosomal protein
- SEQ ID NO:26 DNA sequence for *Staphylococcus aureus* S3 ribosomal protein gene  
(coding and flanking sequences)
- 20 SEQ ID NO:27 Polypeptide sequence for *Staphylococcus aureus* S3 ribosomal protein
- SEQ ID NO:28 DNA sequence for *Staphylococcus aureus* S5 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:29 Polypeptide sequence for *Staphylococcus aureus* S5 ribosomal protein
- SEQ ID NO:30 DNA sequence for *Staphylococcus aureus* S6 ribosomal protein gene  
25 (coding and flanking sequences)
- SEQ ID NO:31 Polypeptide sequence for *Staphylococcus aureus* S6 ribosomal protein
- SEQ ID NO:32 DNA sequence for *Staphylococcus aureus* S9 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:33 Polypeptide sequence for *Staphylococcus aureus* S9 ribosomal protein
- 30 SEQ ID NO:34 DNA sequence for *Staphylococcus aureus* S10 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:35 Polypeptide sequence for *Staphylococcus aureus* S10 ribosomal  
protein

- SEQ ID NO:36 DNA sequence for *Staphylococcus aureus* S11 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:37 Polypeptide sequence for *Staphylococcus aureus* S11 ribosomal  
protein
- 5 SEQ ID NO:38 DNA sequence for *Staphylococcus aureus* S12 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:39 Polypeptide sequence for *Staphylococcus aureus* S12 ribosomal  
protein
- SEQ ID NO:40 DNA sequence for *Staphylococcus aureus* S13 ribosomal protein gene  
10 (coding and flanking sequences)
- SEQ ID NO:41 Polypeptide sequence for *Staphylococcus aureus* S13 ribosomal  
protein
- SEQ ID NO:42 DNA sequence for *Staphylococcus aureus* S14 ribosomal protein gene  
(coding and flanking sequences)
- 15 SEQ ID NO:43 Polypeptide sequence for *Staphylococcus aureus* S14 ribosomal  
protein
- SEQ ID NO:44 DNA sequence for *Staphylococcus aureus* S16 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:45 Polypeptide sequence for *Staphylococcus aureus* S16 ribosomal  
20 protein
- SEQ ID NO:46 DNA sequence for *Staphylococcus aureus* S18 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:47 Polypeptide sequence for *Staphylococcus aureus* S18 ribosomal  
protein
- 25 SEQ ID NO:48 DNA sequence for *Staphylococcus aureus* S19 ribosomal protein gene  
(coding and flanking sequences)
- SEQ ID NO:49 Polypeptide sequence for *Staphylococcus aureus* S19 ribosomal  
protein
- SEQ ID NO:50 DNA sequence for *Staphylococcus aureus* S20 ribosomal polypeptide  
30 gene (coding and flanking sequences)
- SEQ ID NO:51 DNA sequence for *Staphylococcus aureus* S21 ribosomal protein gene  
(coding and flanking sequences)

SEQ ID NO:52 Polypeptide sequence for *Staphylococcus aureus* S21 ribosomal protein

SEQ ID NO:53 Exemplary S4 Forward PCR Primer

SEQ ID NO:54 Exemplary S4 Reverse PCR Primer

5 SEQ ID NO:55 Exemplary S18 Forward PCR Primer

SEQ ID NO:56 Exemplary S18 Reverse PCR Primer

SEQ ID NO:57 Exemplary S6 Forward PCR Primer

SEQ ID NO:58 Exemplary S6 Reverse PCR Primer

SEQ ID NO:59 Exemplary 16S H-44 Helical RNA Forward PCR Primer

10 SEQ ID NO:60 Exemplary 16S H-44 Helical RNA Reverse PCR Primer

SEQ ID NO:61 Exemplary 16S H-7, 8,9,10 & 11 Helical RNA Forward PCR Primer

SEQ ID NO:62 Exemplary 16S H-7, 8,9,10 & 11 Helical RNA Reverse PCR Primer

### Brief Description of the Figures

Figure 1- DNA Coding Region and Amino Acid Sequence of the S20 ribosomal polypeptide

Figure 2. Column Profile of HiPrep SP<sub>XL</sub> Column

Figure 3. Coomassie-stained NuPage Gels of S20 ribosomal polypeptide fractions. Using Novex NuPage™ Bis-gels Tris (4-12%) with a MES Buffer system

Figure 4 Graphic illustration of how specific inhibition of S20 ribosomal polypeptide binding to RNA is detected.

Figure 5 Graphic illustration of a ribosomal assembly map incorporating direct binding S proteins (S4, S8, S7, S17, and S20) as well as some proteins which integrate themselves into ribosomes by reliance on protein-protein interactions (non-direct binding proteins) (S3, S5, S9, S10, S12, S14, S16 and S19). Arrows between proteins indicate the effect of a protein on another whose binding it enhances. Thick arrows indicate a principal contribution. Thin arrows indicate lesser contribution. Noller and Nomura (1987)

Figure 6 Graphical illustration of a ribosomal assembly assay incorporating direct binding S proteins (S4, S8, S7, S17, and S20) as well as proteins which integrate themselves into ribosomes by reliance on protein-protein interactions "non direct binding proteins"(S3, S5, S9, S10, S12, S14, S16 and S19).

## SUMMARY OF THE INVENTION

The present invention provides an isolated *S aureus* S20 ribosomal polypeptide, and the isolated polynucleotide molecules that encode them, as well as vectors and host cells comprising such polynucleotide molecules. The DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded polypeptide, upon expression, can be used as a target for the screening of antibacterial drugs. High-throughput assays for identifying inhibitors of ribosomal assembly are provided. Solid phase high throughput assays are provided, as are related assay compositions, integrated systems for assay screening and other features that will be evident upon review.

In one embodiment, the invention provides an isolated S20 ribosomal polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2. The DNA and predicted amino acid sequence of *Staphylococcus aureus* S20 ribosomal polypeptide is displayed below:

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ATGGCAAATATCAAATCTGCAATTAAACGTGTAAAAACAACCTGAAAAAGCTGAAGCACGC60
M A N I K S A I K R V K T T E K A E A R

AACATTTTCACAAAAGAGTGCAATGCGTACAGCAGTTAAAAACGCTAAACAGCTGTTTCA120
N I S Q K S A M R T A V K N A K T A V S

AATAACGCTGATAATAAAAATGAATTAGTAAGCTTAGCAGTTAAGTTAGTAGACAAAGCT180
N N A D N K N E L V S L A V K L V D K A

GCTCAAAGTAATTTAATACATTCAAACAAAGCTGACCGTATTAAATCACAATTAATGACT240
A Q S N L I H S N K A D R I K S Q L M T

GCAAATAAATAA252
A N K *
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Although SEQ ID NOS:1 and 2 provide particular *S. aureus* sequences, the invention is intended to include within its scope other *S. aureus* allelic variants. Allelic variants are understood to mean naturally-occurring base changes in the species population which may or may not result in an amino acid change of the DNA sequences herein

The present invention also includes include variants of the aforementioned polypeptide, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like characteristics.

5           The nucleic acids of the invention include those nucleic acids coding for the same amino acids in the S20 ribosomal polypeptide due to the degeneracy of the genetic code

          In another embodiment, the invention provides isolated polynucleotides (e.g. RNA and DNA, both naturally occurring and synthetically derived, both single and  
10   double stranded) that comprise a nucleotide sequence encoding the amino acid sequence of the polypeptides of the invention. Such polynucleotides are useful for recombinantly expressing the enzyme and also for detecting expression of the polypeptides in cells (e.g. using Northern hybridization and in situ hybridization assays). Specifically excluded from the definition of polynucleotides of the invention  
15   is the entire isolated chromosome of the native host cells. A preferred polynucleotide of the invention set forth in SEQ ID NO:1 corresponds to the naturally occurring S20 ribosomal polypeptide encoding nucleic acid sequence. It will be appreciated that numerous other sequences exist that also encode S20 ribosomal polypeptide of SEQ ID NO:2 due to the well known degeneracy of the universal genetic code. In another  
20   preferred embodiment the invention is directed to all isolated degenerate polynucleotides encoding the S20 ribosomal polypeptide.

          In another embodiment the invention provides an isolated nucleic acid comprising the nucleotide sequence having least 60%, 70%, 80, 90% identity with SEQ ID NO:1. In one embodiment, the invention provides an isolated S20 ribosomal  
25   polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2.

          In a related embodiment the invention provides vectors comprising a polynucleotide of the invention. Such vectors are useful, e.g. for amplifying the polynucleotides in host cells to create useful quantities thereof. In preferred  
30   embodiments, the vector is an expression vector wherein the polynucleotide of the invention is operatively linked to a polynucleotide comprising an expression control sequence. Such vectors are useful for recombinant production of polypeptides of the invention.

In another related embodiment, the invention provides host cells that are transformed with polynucleotides or vectors of the invention. As stated above, such host cells are useful for amplifying the polynucleotides and also for expressing the S20 ribosomal polypeptide or a fragment thereof encoded by the polynucleotide.

5 In still another related embodiment, the invention provides a method for producing the S20 ribosomal polypeptide (or a fragment thereof) comprising the steps of growing a host cell of the invention in a nutrient medium and isolating the S20 ribosomal polypeptide from the cells.

In still another related embodiment, the invention provides a method for  
10 testing for inhibitors of ribosomal assembly comprising the steps of contacting a labeled S20 ribosomal polypeptide with a ribosomal RNA in the presence and the absence of a test agent, determining the amount of S20 ribosomal polypeptide specifically bound to said RNA both in the presence of a test agent and in the absence of said test agent, and comparing the amount of protein determined in the presence of  
15 the test agent to the amount of protein determined in step in the absence of the test agent.

A decrease in the amount of protein determined in the presence of test agent compared to that determined in the absence of the test agent indicates that said agent is an inhibitor of ribosomal assembly

20 In still another related embodiment, the invention provides a method for testing for inhibitors of ribosomal assembly comprising the steps of contacting at least one direct binding ribosomal polypeptide selected from the group consisting of S4, S7, S8, S15, S17 and S20 with 16S ribosomal RNA in the presence and absence of a test agent and determining the amount of direct binding protein bound to the RNA in  
25 the presence of a test agent; and in the absence of said test agent; and comparing the amount direct binding protein determined under both sets of conditions.

A decrease in the amount of direct binding protein determined in the presence of test agent compared to that determined in the absence of the test agent indicates that said agent is an inhibitor of ribosomal assembly

30 In still another related embodiment the invention provides a method for testing for inhibitors of ribosomal assembly comprising the steps of contacting at least one direct binding ribosomal polypeptide selected from the group consisting of S4, S7, S8, S15, S17 and S20 with 16S ribosomal RNA to form a polyribonucleotide protein

complex and; contacting said polyribonucleotide protein complex with at least one non- direct binding ribosomal polypeptide selected from the group consisting of S1, S2, S3, S5, S6, S9, S10, S11, S12, S13, S14, S16, S18, S19, and S21.

in the presence and absence of a test agent; and then determining the amount of at least one non- direct binding ribosomal polypeptide bound to the RNA in the presence and the absence of a test agent and then comparing the amount of least one non direct binding ribosomal polypeptide bound under both conditions

In still another related embodiment the invention provides an isolated S20 ribosomal polypeptide comprising an amino acid sequence at least 70%, 80, 90%, 95% identical to the sequence of SEQ ID NO:2.

In addition to the foregoing, the invention includes as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations specifically mentioned above. Although the applicant(s) invented the full scope of the claims appended hereto, the claims appended are not intended to encompass within their scope the prior art work of others. Therefore, in the event that statutory prior art within the scope of a claim is brought to the attention of the applicants by a Patent Office or other entity or individual, the applicant(s) reserve the right to exercise amendment rights under applicable patent laws to redefine the subject matter of such a claim to specifically exclude such statutory prior art or obvious variations of statutory prior art from the scope of such a claim. Variations of the invention defined by such amended claims also are intended as aspects of the invention.

### **DETAILED DESCRIPTION OF THE INVENTION**

The foregoing is provided to further facilitate understanding of the applicant's invention but is not intended to limit the scope of applicant's invention.

#### **Definitions**

As used hereinafter "Isolated" means altered by the hand of man from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

As used hereinafter "Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or

DNA or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that  
5 may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include,  
10 for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short  
15 polynucleotides, often referred to as oligonucleotides.

As used hereinafter "Polypeptide" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally  
20 referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research  
25 literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of  
30 ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a



heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, *Proteins-Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, pgs. 1-12 in *Postranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter et al., "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol* (1990) 182:626-646 and Rattan et al., "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci* (1992) 663:4842).

As used hereinafter "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

As used hereinafter "Identity" is a measure of the identity of nucleotide sequences or amino acid sequences. In general, the sequences are aligned so that the highest order match is obtained. "Identity" per se has an art-recognized meaning and can be calculated using published techniques (see, e.g.: *Computational Molecular Biology*, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part I*, Griffin, A. M., and Griffin, H. G., eds., Humana Press, N.J., 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (Carillo, H., and Lipton, D., *SIAM J Applied Math* (1988) 48:1073). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in *Guide to Huge Computers*, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H., and Lipton, D., *SIAM J Applied Math* (1988) 48:1073. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux, J., et al., *Nucleic Acids Research* (1984) 12(1):387), BLASTP, BLASTN, and FASTA (Atschul, S. F. et al., *J Molec Biol* (1990) 215:403). The well known Smith Waterman algorithm may be used to determine identity. The Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison, Wisconsin) is one such program which uses the algorithm of Smith and Waterman (*Adv. Appl. Math.* 2:482-489 (1981)).

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:1, that is be 100% identical, or it may include up to a certain integer number of nucleotide alterations as compared to the reference sequence. Such alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in

one or more contiguous groups within the reference sequence. The number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO:1 by the numerical percent of the respective percent identity (divided by 100) and subtracting that product from said total number of nucleotides in SEQ ID

5 NO:1, or:

$$n_n \leq x_n - (x_n \cdot y)$$

wherein  $n_n$  is the number of nucleotide alterations,  $x_n$  is the total number of nucleotides in SEQ ID NO:1, and  $y$  is 0.50 for 50%, 0.60 for 60%, 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and wherein any non-integer product of  $x_n$  and  $y$  is rounded down to the nearest integer prior to subtracting it from  $x_n$ . Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:2 may create nonsense, missense or

15 frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

Similarly, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:2, that is be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference

20 sequence such that the % identity is less than 100%. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed

25 either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NO:2 by the numerical percent of the respective percent identity (divided by 100) and then subtracting that product from said total number of

30 amino acids in SEQ ID NO:2, or:

$$n_a \leq x_a - (x_a \cdot y)$$

wherein  $n_a$  is the number of amino acid alterations,  $x_a$  is the total number of amino acids in SEQ ID NO:2, and  $y$  is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and wherein any non-integer product of  $x_a$  and  $y$  is rounded down to the nearest integer prior to subtracting it from  $x_a$ . Identity has been similarly defined in  
5 US Patent No. 6,083,924 which is hereby incorporated by reference.

The present invention provides isolated polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single and double stranded) encoding a *Staphylococcus aureus* ribosomal protein S20. The nucleic acids of the invention include those nucleic acids coding for the same amino  
10 acids in the S20 ribosomal polypeptide due to the degeneracy of the genetic code. DNA polynucleotides of the invention include genomic DNA and DNA that has been synthesized in whole or in part. "Synthesized" as used herein and understood in the art, refers to polynucleotides produced by purely chemical as opposed to enzymatic methods. "Wholly" synthesized DNA sequences are therefore produced entirely by  
15 chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Genomic DNA of the invention comprises the protein-coding region for a polypeptide of the invention and is also intended to include allelic variants. Allelic variants are understood to mean naturally-occurring base changes in  
20 the species population which may or may not result in an amino acid change of the DNA sequences herein.

"16S ribosomal RNA" is understood to mean an isolated small subunit RNA of any prokaryote whether isolated from ribosomes, made synthetically or prepared by transcription, "16S ribosomal RNA" can mean either the full length sequence or a  
25 fragment thereof.

As used herein, the term "contacting" means bringing together, either directly or indirectly, a compound into physical proximity to a polypeptide or polynucleotide of the invention. Additionally "contacting" may mean bringing a polypeptide of the invention into physical proximity with another polypeptide or polynucleotide (either  
30 another polypeptide or polynucleotide of the invention or a polypeptide or polynucleotide not so claimed) or bringing a polynucleotide of the invention into physical proximity with a polypeptide or polynucleotide (either a polypeptide or polynucleotide of the invention or a polypeptide or polynucleotide not so claimed).

As used herein, the term "polyribonucleotide protein complex" refers to a covalent or non-covalently associated molecular entity containing 16S ribosomal RNA and at least one small subunit ribosomal protein

"Small subunit ribosomal protein" as used herein refers to ribosomal proteins present in the small (30S) ribosomal subunit of the ribosome of derived from any prokaryotic species. Small subunit ribosomal proteins include: S1, S2 S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, and S21.

"Direct binding ribosomal polypeptide" or "direct binding S-protein" or "direct binding ribosomal protein" or "direct binding protein" as used herein refers to a polypeptide derived from any prokaryotic species selected from the group consisting of S4, S7, S8, S17, S15 and S20

"Non- direct binding ribosomal polypeptide" or "non direct binding S-protein" or "non direct binding ribosomal protein" or "non-direct binding protein" as used herein refers to a polypeptide derived from any prokaryotic species selected from the group consisting of S1, S2 S3, S5, S6, S9, S10, S11, S12, S13, S14, S16, S18, S19, and S21. These proteins are also referred to as "secondary binding proteins".

"Antibodies" as used herein includes monoclonal and polyclonal antibodies, chimeric, single chain, simianized antibodies and humanized antibodies, as well as Fab fragments, including the products of an Fab immunoglobulin expression library. The S20 ribosomal polypeptides of the invention or variants thereof, or cells expressing them can be used as an immunogen to produce antibodies immunospecific for such polypeptides.

#### **Nucleic Acids of the Invention**

A preferred DNA sequence of the invention encoding the *Staphylococcus aureus* S20 ribosomal polypeptide is set out in SEQ ID NO:1. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example the molecule having the sequence set forth in SEQ ID NO:1 along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO:1 according to Watson-Crick base pairing rules for DNA. Also preferred are other polynucleotides encoding the S20 ribosomal polypeptide of SEQ ID NO:2, which differ in sequence from the polynucleotide of SEQ ID NO:1 by virtue of the well-

known degeneracy of the universal genetic code. The determination of the nucleotide sequence is described in the following example.

### Example 1

#### 5     **Procedure for obtaining sequence information of the S20 gene directly from the 2.8 Mb *S. aureus* genome.**

The *S. aureus* S20 gene was sequenced using an ABI377 fluorescence-based sequencer (Perkin Elmer/Applied Biosystems Division, PE/ABD, Foster City, CA) and the ABI PRISM™ Ready Dye-Deoxy Terminator kit with *Taq* FS™ polymerase.

10   Each ABI cycle sequencing reaction contained about 4 µg of Qiagen purified *S. aureus* genomic DNA, 100 ng of primer, and in a 2X standard reaction volume (40 µl total volume). Cycle-sequencing was performed using an initial denaturation at 98°C for 1 min, followed by 100 cycles: 98°C for 30 sec, annealing at 50°C for 30 sec, and extension at 60°C for 4 min. Temperature cycles and times were controlled by a

15   Perkin-Elmer 9700 thermocycler. Extension products were purified using Centriflex™ gel filtration cartridges (Advanced Genetic Technologies Corp., Gaithersburg, MD). Each reaction product was loaded by pipette onto the column, which was then centrifuged in a swinging bucket centrifuge (Sorvall model RT6000B table top centrifuge) at 1500 x g for 4 min at room temperature. Column-purified

20   samples were dried under vacuum for about 40 min and then dissolved in 1.5 µl of a DNA loading solution (83% deionized formamide, 8.3 mM EDTA, and 1.6 mg/ml Blue Dextran). The samples were then heated to 90°C for three min and the complete sample was loaded into the gel sample well of the ABI377 sequencer. Sequence analysis was done by importing ABI377 files into the Sequencher program (Gene

25   Codes, Ann Arbor, MI). Generally sequence reads of 600 bp were obtained. Sequence base call ambiguities were removed by obtained the complete sequence of each gene on both DNA strands.

#### **Sequencing of the *S. aureus* S20 gene.**

Partial DNA sequences encoding a portion of *S. aureus* S20 ribosomal

30   polypeptide have been described. Human Genome Sciences ID #V76479 and TIGR # TI:GSA\_604 The TIGR sequence matches the first 79 nucleotides of the sequence disclosed in this invention. The Human Genome Sciences, Inc. sequence contains 109 nucleotides which codes for the carboxy terminal 35 amino acid residues. The

combination of the TIGR and HGS partial S20 ribosomal polypeptide gene sequences do not overlap as they contain a 63 nucleotide gap. The invention provides a complete sequence. The *Bacillus subtilis* ribosomal S20 polypeptide shares some identity with the *S. aureus* S20 ribosomal polypeptide; however the proteins differ by  
5 about 52% identity in their protein sequences.

The 187 bp GST in the TIGR database (TI:GSA\_604) encodes about 26 amino acids of the *S. aureus* S20 ribosomal polypeptide gene. starting with the Met codon. This sequence, of unknown quality, was used to design three forward primers, SEQ ID NO:3 (5'AATATCAAATCTGCAATTAAACG)  
10 SEQ ID NO:4 (5'AAATTTTGATAAGATGAACTCAC) and  
SEQ ID NO:5 (5'TTTAGGAGGTGACAGAAATGGC) . Only one of these primers generated any useful new sequence data, SEQ ID NO:3 primed a poor sequence read of about 400 bp. A second attempt using primer SEQ ID NO:3 produced a higher quality read that extended about 600 bp. Both reads were used to design three  
15 additional primers, forward primer SEQ ID NO:6 .  
(5'ACGCAACATTTTCACAAAAGAGTGC)  
and reverse primer SEQ ID NO:7 (5'- ATTGCACTCTTTTGTGAAATGTTGC) and  
SEQ ID NO:8 (5'- ATCTTTATAAAAAATAAAAGTTC). Excellent sequence reads of more than 500 bp. were obtained from primers SEQ ID NO:6 and SEQ ID NO:7  
20 and a poor quality, but usable, read was obtained from primer SEQ ID NO:8. The combined four reads provided the complete double-stranded sequence of the *S.aureus* S20 ribosomal polypeptide gene region. Thus, the goal to obtain the complete accurate sequence of the *S. aureus* S20 ribosomal polypeptide gene directly from the genome was achieved. A total of 1.2 kb of sequence data was obtained within and  
25 around the S20 ribosomal polypeptide gene.

The invention further embraces species, which are homologs of the *Staphylococcus aureus* S20 ribosomal polypeptide encoding DNA. Species homologs, would encompass nucleotide sequences which share at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%,  
30 at least 98%, at least 99% identity with *Staphylococcus aureus* polynucleotide of the invention

The polynucleotide sequence information provided by the invention makes possible large scale expression of the encoded polypeptide by techniques well known

and routinely practiced in the art. Polynucleotides of the invention also permit identification and isolation of polynucleotides encoding related ribosomal proteins, such as allelic variants and species homologs, by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR).

5           The disclosure herein of a full length polynucleotide encoding an S20 ribosomal polypeptide makes readily available to the worker of ordinary skill in the art every possible fragment of the full length polynucleotide. The invention therefore provides fragments of the S20 ribosomal polypeptide encoding polynucleotides comprising at least 14-15, and preferably at least 18, 20, 25, 50, or 75 consecutive  
10       nucleotides of a polynucleotide encoding S20 ribosomal polypeptide. Preferably, fragment polynucleotides of the invention comprise sequences unique to the S20 ribosomal polypeptide encoding polynucleotide sequence and therefore hybridize under highly stringent or moderately stringent conditions only (i.e. "specifically") to polynucleotides encoding S20 ribosomal polypeptide. Sequences unique to  
15       polynucleotides of the invention are recognizable through sequence comparison to other known polynucleotides, and can be identified through use of alignment programs routinely utilized in the art, e.g. those made available in public sequence databases. Such sequences are also recognizable from Southern hybridization analyses to determine the number of fragments of genomic DNA to which a  
20       polynucleotide will hybridize. Polynucleotides of the invention can be labelled in a manner that permits their detection, including radioactive, fluorescent, and enzymatic labelling.

          Fragment polynucleotides are particularly useful as probes for detection of full length or other fragment S20 ribosomal polypeptide polynucleotides or for the  
25       expression of fragments of S20 ribosomal polypeptide. One or more fragment polynucleotides can be included in kits that are used to detect variations in a polynucleotide sequence encoding S20 ribosomal polypeptide.

          The invention also embraces DNAs encoding S20 ribosomal polypeptide polypeptides which DNAs hybridize under moderately stringent or high stringency  
30       conditions to the non-coding strand, or complement, of the polynucleotide in SEQ ID NO:1

          Exemplary highly stringent hybridization conditions are as follows:  
hybridization at 42°C in a hybridization solution comprising 50% formamide, 1%



SDS, 1M NaCl, 10% Dextran sulfate, and washing twice for 30 minutes at 60°C in a wash solution comprising 0.1 X SSC and 1% SDS. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described Ausubel, et al. (Eds.), Protocols in  
5 Molecular Biology, John Wiley & Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, et al., (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory  
10 Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

### **Host Cells and Vectors of the Invention**

According to another aspect of the invention, host cells are provided, including prokaryotic and eukaryotic cells, comprising a polynucleotide of the invention (or vector of the invention) in a manner which permits expression of the encoded S20  
15 ribosomal polypeptide. Polynucleotides of the invention may be introduced into the host cell as part of a circular plasmid, or as linear DNA comprising an isolated protein coding region or a viral vector. Methods for introducing DNA into the host cell well known and routinely practiced in the art include transformation, transfection, electroporation, nuclear injection, or fusion with carriers such as liposomes, micelles,  
20 ghost cells, and protoplasts. Expression systems of the invention include bacterial, yeast, fungal, plant, insect, invertebrate, and mammalian cells systems. Suitable host cells for expression of S20 ribosomal polypeptides include prokaryotes, yeast, and higher eukaryotic cells. Suitable prokaryotic hosts to be used for the expression of human *Staphylococcus aureus* Ribosomal Protein Gene, S20 include  
25 bacteria of the genera *Escherichia*, *Bacillus*, and *Salmonella*, as well as members of the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*.

The isolated nucleic acid molecules of the invention are preferably cloned into a vector designed for expression in prokaryotic cells, rather than into a vector designed for expression in eukaryotic cells. Prokaryotic cells are preferred for  
30 expression of genes obtained from prokaryotes because prokaryotic cells are more economical sources of protein production and because prokaryotic hosts grow to higher density and are typically grown in media which is less expensive than that used for the growth of eukaryotic hosts.

In the event a eukaryotic host were used the possibilities may include, but are not limited to, the following: insect cells, African green monkey kidney cells (COS cells), Chinese hamster ovary cells (CHO cells), human 293 cells, and murine 3T3 fibroblasts.

5        Expression vectors for use in prokaryotic hosts generally comprise one or more phenotypic selectable marker genes. Such genes generally encode, *e.g.*, a protein that confers antibiotic resistance or that supplies an auxotrophic requirement. A wide variety of such vectors are readily available from commercial sources. Examples include pSPORT vectors, pGEM vectors (Promega), pPROEX vectors  
10        (LTI, Bethesda, MD), Bluescript vectors (Stratagene), and pQE vectors (Qiagen). A representative cloning and expression scheme is provided by the following example.

### Example 2

#### Isolation and Cloning of the S20 Coding Region

Two primers were designed for PCR. SEQ ID NO:9 (GTGTT ATCGATA  
15        ATGGCAAATATCAAATCTGCAATTAAACG)

This sequence includes an overhang (GTGTT), a *ClaI* site, the start codon and the next 26 bases of the S20 ribosomal polypeptide gene and  
SEQ ID NO:10 (5' GTGTTGGATCC TTA TTT ATT TGC AGT CAT TAA TTG  
TG). This sequence includes an overhang (GTGTT), a *BamHI* site, the stop codon  
20        and the next 23 bases of S20 *S. aureus* ribosomal protein.

Staphylococcus aureus genomic DNA was used as a template. The buffer (N808-0006) and Amplitaq® (N8080-0101) were purchased from Perkin Elmer Cetus. The 10 mM dNTP mix was obtained from Gibco BRL (Gaithersburg, MD). The reaction mix was 5 µl of buffer, 1 µl of dNTP mix, 1 ng of each primer, 1 ng of genomic DNA  
25        and 0.5 µl (2.5 units) of amplitaq in a final volume of 50 µl.

The program for PCR was 94°C for 10 minutes and then 40 cycles of 94°C for 1 minute, 57°C for 30 seconds, and 72°C for one minute. The final extension phase was at 72°C for 3 minutes and the reactions were allowed to stay at 4°C until they were removed from the thermocycler.

#### 30        Vector Construction and Expression

The PCR products were purified, digested with *ClaI* and *BamHI* and ligated to the expression vector pSR-Tac which contains *ClaI* and *BamHI* cloning sites. This vector contains a tac promoter, an AT rich synthetic ribosome binding site, two

transcription terminators designated T1 and sib3 upstream of the tac promoter and downstream of the cloned gene, respectively, an ampicillin resistance gene derived from pBR322, and a ColE1 origin of replication. The Cla I restriction site is located immediately downstream of the ribosome binding site and the BamHI site is immediately upstream of the sib3 terminator. While this particular vector worked quite well it is expected that other vectors used in *E.coli* heterologous protein expression would be equally suitable.

After transformation into *E. coli* strain Top10 F' *lacI*<sup>q</sup>, the colonies were screened by DNA mini prep and restriction digestion to find the desired constructs. The constructs were sequenced and transformed into *E. coli* strain K12s F' *lacI*<sup>q</sup> for expression studies.

Cells harboring the construct pSRTac-S20 were grown in 50 ml LB with ampicillin at 37°C. The cultures were induced with 10<sup>-3</sup> M IPTG during the midlog phase of growth and allowed to express for 3 hours. Then the cells were collected, sonicated and examined using gel electrophoresis.

Half a milliliter of the sonicated expression cultures were centrifuged at 10,000 rpm for 10 minutes. The supernatant was collected as the soluble fraction and the pellet (insoluble fraction) was suspended in 10 mM Tris-HCl pH 8.0. These samples were electrophoresed on 20% acrylamide with DATD crosslinker. The S20 protein was expressed at moderate levels and observed to be in the soluble fraction.

### **Polypeptides of the Invention**

Overexpression in eukaryotic and prokaryotic hosts as described above facilitates the isolation of S20 polypeptides. The invention therefore includes isolated S20 polypeptides as set out in SEQ ID NO:2 and variants and conservative amino acid substitutions therein including labeled and tagged polypeptides.

The invention includes S20 polypeptides which are "labeled". The term "labeled" is used herein to refer to the conjugating or covalent bonding of any suitable detectable group, including enzymes (e.g., horseradish peroxidase, beta-glucuronidase, alkaline phosphatase, and beta-D-galactosidase), fluorescent labels (e.g., fluorescein, luciferase), and radiolabels (e.g., <sup>14</sup>C, <sup>125</sup>I, <sup>3</sup>H, <sup>32</sup>P, and <sup>35</sup>S) to the compound being labeled. Techniques for labeling various compounds, including proteins, peptides, and antibodies, are well known. See, e.g., Morrison, *Methods in Enzymology* 32b, 103 (1974); Syvanen et al., *J. Biol. Chem.* 284, 3762 (1973);

Bolton and Hunter, *Biochem. J.* 133, 529 (1973). The termed labelled may also encompass a polypeptide which has covalently attached an amino acid tag as discussed below.

In addition, the S20 polypeptides of the invention may be indirectly labeled.

- 5 This involves the covalent addition of a moiety to the polypeptide and subsequent coupling of the added moiety to a label or labeled compound which exhibits specific binding to the added moiety. Possibilities for indirect labeling include biotinylation of the peptide followed by binding to avidin coupled to one of the above label groups. Another example would be incubating a radiolabeled antibody specific for a  
10 histidine tag with a S20 polypeptide comprising a polyhistidine tag. The net effect is to bind the radioactive antibody to the polypeptide because of the considerable affinity of the antibody for the tag.

The invention also embraces variants (or analogs) of the S20 protein. In one example, insertion variants are provided wherein one or more amino acid residues  
15 supplement a S20 amino acid sequence. Insertions may be located at either or both termini of the protein, or may be positioned within internal regions of the S20 protein amino acid sequence. Insertional variants with additional residues at either or both termini can include for example, fusion proteins and proteins including amino acid tags or labels. Insertion variants include S20 polypeptides wherein one or more  
20 amino acid residues are added to a S20 acid sequence, or to a biologically active fragment thereof.

Insertional variants therefore can also include fusion proteins wherein the amino and/or carboxy termini of S20 is fused to another polypeptide. Various tag polypeptides and their respective antibodies are well known in  
25 the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the influenza HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD)  
30 tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag -peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an alpha -tubulin epitope peptide [Skinner et al.,

J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397(1990)]. In addition, the S20 polypeptide can be tagged with enzymatic proteins such as peroxidase and alkaline phosphatase.

5 In another aspect, the invention provides deletion variants wherein one or more amino acid residues in a S20 polypeptide are removed. Deletions can be effected at one or both termini of the S20 polypeptide, or with removal of one or more residues within the S20 amino acid sequence. Deletion variants, therefore, include all fragments of the S20 polypeptide.

10 The invention also embraces polypeptide fragments of the sequence set out in SEQ ID NO: 2 wherein the fragments maintain biological (e.g., ligand binding or RNA binding and/or other biological activity) Fragments comprising at least 5, 10, 15, 20, 25, 30, 35, or 40 consecutive amino acids of SEQ ID NO: 2 are comprehended by the invention. Fragments of the invention having the desired  
15 biological properties can be prepared by any of the methods well known and routinely practiced in the art.

The present invention also includes include variants of the aforementioned polypeptide, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like  
20 characteristics. Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that  
25 has similar properties. Exemplary conservative substitutions are set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

**Table A**

**Conservative Substitutions I**

30

<b>SIDE CHAIN CHARACTERISTIC</b>	<b>AMINO ACID</b>
--------------------------------------	-------------------

**Aliphatic**

Non-polar

G A P

I L V

Polar - uncharged

C S T M

5

N Q

Polar - charged

D E

K R

Aromatic

H F W Y

Other

N Q D E

10

Alternatively, conservative amino acids can be grouped as described in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B, immediately below

**Table B**

15

**Conservative Substitutions II****SIDE CHAIN****CHARACTERISTIC****AMINO ACID**

20

Non-polar (hydrophobic)

A. Aliphatic:

A L I V P

B. Aromatic:

F W

C. Sulfur-containing:

M

D. Borderline:

G

25

Uncharged-polar

A. Hydroxyl:

S T Y

B. Amides:

N Q

C. Sulfhydryl:

C

D. Borderline:

G

30

Positively Charged (Basic):

K R H

Negatively Charged (Acidic):

D E

As still an another alternative, exemplary conservative substitutions are set out in Table C, immediately below.

Table C

5	Conservative Substitutions III	
	<u>Original Residue</u>	<u>Exemplary Substitution</u>
	Ala (A)	Val, Leu, Ile
	Arg (R)	Lys, Gln, Asn
10	Asn (N)	Gln, His, Lys, Arg
	Asp (D)	Glu
	Cys (C)	Ser
	Gln (Q)	Asn
15	Glu (E)	Asp
	His (H)	Asn, Gln, Lys, Arg
	Ile (I)	Leu, Val, Met, Ala, Phe,
	Leu (L)	Ile, Val, Met, Ala, Phe
	Lys (K)	Arg, Gln, Asn
20	Met (M)	Leu, Phe, Ile
	Phe (F)	Leu, Val, Ile, Ala
	Pro (P)	Gly
	Ser (S)	Thr
	Thr (T)	Ser
25	Trp (W)	Tyr
	Tyr (Y)	Trp, Phe, Thr, Ser
	Val (V)	Ile, Leu, Met, Phe, Ala

Generally it is anticipated that the S20 polypeptide will be found primarily  
 30 intracellularly, the intracellular material can be extracted from the host cell using  
 any standard technique known to the skilled artisan. For example, the host cells can  
 be lysed to release the contents of the periplasm/cytoplasm by French press,

homogenization, and/or sonication followed by centrifugation. The S20 polypeptide is found primarily in the supernatant after centrifugation of the cell homogenate, and the S20 polypeptide can be isolated by way of non-limiting example by any of the methods below.

5           In those situations where it is preferable to partially or completely isolate the S20 polypeptide, purification can be accomplished using standard methods well known to the skilled artisan. Such methods include, without limitation, separation by electrophoresis followed by electroelution, various types of chromatography (immunoaffinity, molecular sieve, and/or ion exchange),  
10       and/or high pressure liquid chromatography. In some cases, it may be preferable to use more than one of these methods for complete purification.

          Purification of S20 polypeptide can be accomplished using a variety of techniques. If the polypeptide has been synthesized such that it contains a tag such as Hexahistidine (S20/hexaHis) or other small peptide such as FLAG (Eastman  
15       Kodak Co., New Haven, Conn.) or myc (Invitrogen, Carlsbad, Calif.) at either its carboxyl or amino terminus, it may essentially be purified in a one-step process by passing the solution through an affinity column where the column matrix has a high affinity for the tag or for the polypeptide directly (i.e., a monoclonal antibody specifically recognizing S20). For example, polyhistidine binds with great affinity and  
20       specificity to nickel, thus an affinity column of nickel (such as the Qiagen Registered TM nickel columns) can be used for purification of S20/polyHis. (See for example, Ausubel et al., eds., Current Protocols in Molecular Biology, Section 10.11.8, John Wiley & Sons, New York [1993]).

          Even if the S20 polypeptide is prepared without a label or tag to facilitate  
25       purification. The S20 of the invention may be purified by immunoaffinity chromatography. To accomplish this, antibodies specific for the S20 polypeptide must be prepared by means well known in the art. Antibodies generated against the S20 polypeptides of the invention can be obtained by administering the polypeptides or epitope-bearing fragments, analogues or cells to an animal, preferably a  
30       nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Kohler, G. and Milstein, C., Nature 256: 495-497 (1975); Kozbor et al., Immunology Today



4: 72 (1983); Cole et al., pg. 77-96 in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985).

Where the S20 polypeptide is prepared without a tag attached, and no  
5 antibodies are available, other well known procedures for purification can be used. Such procedures include, without limitation, ion exchange chromatography, molecular sieve chromatography, HPLC, native gel electrophoresis in combination with gel elution, and preparative isoelectric focusing ("Isoprime" machine/technique, Hoefer Scientific). In some cases, two or more of these techniques may be  
10 combined to achieve increased purity. A representative purification scheme is detailed below.

### **Example 3** **Large Scale Purification of S20 Protein**

S20-expressing *E. coli* cell paste resulting from 6 liters of fermentation was  
15 resuspended in ~ 70 mL Tris buffer pH 7.4 containing 1 mM MgCl<sub>2</sub> and 1 mM DTT. One Complete<sup>®</sup> EDTA-free protease inhibitor pellet (Boehringer Mannheim, Indianapolis, IN) was added to the suspended cells. The cells were lysed by passage three times through a French Press @ 10,000 PSI. A soluble fraction was prepared from the cellular lysate by ultracentrifugation @ 100,000 x g for 60 minutes @ 4<sup>0</sup> C.  
20 The soluble fraction was injected onto a HiPrep SP<sub>XL</sub> 16/10 cation exchange column which had been equilibrated in 50 mM Tris buffer pH 7.4, 1 mM MgCl<sub>2</sub>, and 1 mM DTT. The column flow rate was 4 mL/min. The column was washed with buffer until the Abs<sub>280</sub> of the column eluate was less than 0.01. Material was eluted off of the HiPrep SP<sub>XL</sub> column with a linear gradient of 0-700 mM NaCl in column buffer over  
25 20 column volumes. The column profile is shown in Figure 2. Fractions were collected and analyzed by SDS-PAGE using 4-12% Bis-Tris NuPage<sup>®</sup> gels (Novex, San Deigo, CA) employing a MES buffer system. The gel is shown in figure 3. The gel legend is shown below.

30

Key to S20 Gel			
Lane	Sample	Lane	Sample
1	MW Standards	11	Fraction 32
2	Crude Lysate	12	MW Standards
3	Fraction 25	13	Fraction 33
4	Fraction 26	14	Fraction 34
5	Fraction 27	15	Fraction 35
6	Fraction 28	16	Fraction 36
7	Fraction 29	17	Fraction 37
8	Fraction 30	18	Fraction 38
9	Fraction 31	19	Fraction 39
10	MW Standards	20	MW Standards

S20-containing fractions were further analyzed by liquid chromatography electrospray mass spectrometry (LC/MS-ESI) performed on a Finnigan LC/Q instrument. The results of the LC/MS-ESI analysis yielded an average mass of 8064 amu which would correspond to a *des*<sup>9</sup> form of *S. aureus* ribosomal protein S20. The calculated average mass of the intact S20 is calculated to be 9021.46. The calculated average mass of the *des*<sup>9</sup> form of S20 is 8064.25. The sequence of *S. aureus* S20 is shown below. The *des*<sup>9</sup> form of the protein is highlighted in bold type.

MANIKSAIKRVKTTEKAEARNISQKSAMRTAVKNAKTAVSNNADNKNELVSLAVKLVD  
 KAAQSNLIHSNKADRIKSQQLMTANK

In addition to preparing and purifying S20 polypeptide using recombinant DNA techniques, the S20 polypeptides, fragments, and/or derivatives thereof may be prepared by chemical synthesis methods (such as solid phase peptide synthesis) using techniques known in the art such as those set forth by Merrifield et al., (J. Am. Chem. Soc., 85:2149 [1963]), Houghten et al. (Proc Natl Acad. Sci. USA, 82:5132 [1985]), and Stewart and Young (Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, Ill. [1984]). Such polypeptides may be synthesized with or without a methionine on the amino terminus. Chemically synthesized S20 polypeptides or fragments may be oxidized using methods set forth in these references to form disulfide bridges. The S20 polypeptides or fragments are expected to have biological activity comparable to S20 polypeptides produced recombinantly or purified from natural sources, and thus may be used interchangeably with recombinant or natural S20 polypeptide.

**Ribosomal Assembly Assays**

70S ribosome particles in *E.coli* consist of 31 core ribosomal "L" proteins and two rRNAs (5S and 23S) in the 50S subunit and 21 "S" proteins and a single 16S rRNA in the 30S subunit. These particles constitute the basic machinery for bacterial protein translation. It is postulated that the *Staphylococcus aureus* ribosome is assembled in fashion to ribosomes in *E.coli*. The present invention provides several methods to study the *S.aureus* 30S subunit assembly and methods to screen for inhibitors of the assembly process.

Assembly of the 30S ribosomal subunit is an ordered process both *in vivo* and *in vitro*. Nomura, M. and Held, W.A. (1974), Noller and Nomura (1987). It is now well known that the 21 proteins which comprise the the *E. coli* 30S subunit assemble onto the the 16S rRNA in an ordered fashion *in vitro*. *Id.* These proteins have been defined as primary or secondary binders, according to whether they bind to the 16S RNA independently of other proteins or not. Proteins that bind directly to 16S rRNA include S4, S7, S8, S15, S17 and S20. Secondary binding proteins include S3, S5, S9, S10, S12, S14, S16 and S19.

Producing and purifying the *S.aureus* ribosomal "S" proteins which are most critical for the formation of functional 30S subunits including those that bind directly to 16S rRNA (i.e., S4, S7, S8, S15, S17 and S20) "direct binding S-proteins" and critical proteins that integrate themselves into the ribosome by reliance on protein-protein and/or protein-RNA interactions (non-direct binding S- proteins)(S3, S5, S9, S10, S12, S14, S16 and S19) provides myriad choices in designing methods for testing inhibitors of ribosomal assembly.

**16S RNA binding assay for ribosomal protein S20**

Because S20 is a direct binding S protein it makes possible an assay in which S20 binding to 16S RNA may be measured directly. Such an assay involves the incubation of S20 polypeptide with 16S RNA, separation of bound from unbound S20 and measurement of that fraction of the S20 that remains bound to the RNA. By way of non-limiting example one can envision numerous ways in which the presence of unbound or bound S20 could be detected. The S20 might be radiolabeled in any of a number of means including but not limited to, labeling *in vitro* by chemical or enzymatic means or *vivo* by metabolically labeling cells expressing S20.

As discussed above commonly used radioactive isotopes used for the radiolabeling of peptides and proteins and nucleic acids include but are not limited to

<sup>3</sup>H, <sup>14</sup>C, <sup>35</sup>S, <sup>125</sup>I and <sup>32</sup>P. In addition, of course, if the S20 polypeptide or is tagged with an amino acid tag, as described above, the tag and the covalently attached S20 protein can be detected by means well known in the art. In addition, the S20 polypeptide or a polynucleotide can be tagged with enzymatic proteins such as  
5 peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) which are capable of being monitored for change in fluorescence intensity, wavelength shift, or fluorescence polarization (FP) or fluorescent resonance energy transfer (FRET). Another method of labeling polypeptides and nucleic acids includes biotinylation of the peptide of the peptide or nucleic acid  
10 followed by binding to avidin coupled to one of the above label groups or a solid support. In addition of course, such an assay is amenable to being performed with the 16S RNA (or a fragment thereof) being labeled with a radiolabel, a tag, or indirectly with a molecule such as biotin. The assay may be performed entirely in solution phase or it may be performed with either the 16S RNA or the 20S  
15 polypeptide immobilized. A common means of immobilization is to attach biotin to the molecule of interest and immobilize it by contacting with a solid support to which avidin is bound. By way of non-limiting example, an assay in which the S20 polypeptide is immobilized on a solid support and is used to bind radiolabeled 16S RNA and an assay in which all components are free in solution are described below.

20

#### Example 4

##### 16S RNA -S20 binding assay

Because S20 is known to bind directly to 16S rRNA isolated S20 protein is an important reagent for developing a protein:RNA binding assay. The reagents for such a screen include S20 protein and labeled 16S RNA or a fragment of 16S RNA  
25 capable of binding the S20 polypeptide. Depending on the format of the assay, the S20 polypeptide or the 16S RNA may be labeled by means of radiolabeling or with tags which make the RNA or polypeptide amenable to immobilization to a solid support.

##### Preparation of Starting Materials

##### 30 Cloning of 16S Ribosomal RNA

The complete 16S-rRNA gene was identified in the HGS data base on contig 168268 by homology to the *B. subtilis* sequence. Five prime sequence of 5'-TTTATGGAGAGTTTGATCCTGGC-3' and the 3' sequence of 5'-GCGGCTGGATCACCTCCTTTCT-3' is used to amplify the entire 16S-rRNA gene

from *S. aureus* (Oligo Etc; Wilsonville, OR). The amplified gene is cloned into pT7Blue using Novagen's (Madison, WI) Perfectly Blunt Cloning Kit. DNA template is created by PCR using a primer that had the T7 promoter on the 5' end sequence of the 16S-rRNA gene (5'-TAATACGACTCACTATAGTTTATGGA-  
 5 GAGTTTGATCCTGGC-3'). The length of the amplified 16S-rRNA fragment can be altered by the selection of the 3' primer. Whole 16S-rRNA as well as shorter segments could be used for screening of S20-16S-rRNA antagonists. The crystal structure has been solved for the 30S subunit (Brian T. Wimberly, et al Structure of the 30S ribosomal subunit. *Nature*. vol 407; p327-338, 2000). Helical pieces, H8,  
 10 H9, H11, and H44 create a pocket for the S20 protein to bind. These smaller helical pieces can be used for screen of S20 antagonist. Fragmented segments can be generated with the same T7 promoter as the whole 16S-rRNA was created and can also be labeled.

Helical RNAs	5'	3'
H-44 Nucleotide 1419-1502 SEQ ID NO:21	CACCACGAGAGTTTGTAAC (SEQ ID NO:59)	CACCCCAATCATTGTGCCAC (SEQ ID NO:60)
H-7,8,9,10,& 11 Nucleotide 120-322 SEQ ID NO:21	CACGTGGATAACCTACCTA (SEQ ID NO:61)	GTGGCCGATCACCTCTCAGG (SEQ ID NO:62)

15 <sup>3</sup>H-UTP or <sup>35</sup>S-ATP can be used to label the RNA if labeled RNA is desired. Resulting RNAs are characterized by electrophoresis on acrylamide-urea gels, and RNA concentrations are determined by UV spectroscopy using A<sub>260</sub> unit = 40 ug/ml. The entire S16 ribosomal RNA gene sequence has been reported (Genbank Accession  
 20 # X68417 also US Patent No. 5,843,669 Sequence # 160). The sequence of the gene is included in this document as SEQ ID NO:21

#### *Biotinylation of S20*

Purified S20 is biotinylated with the Pierce EZ-link Sulfo-NHS-LC-Biotinylation Kit (Pierce, Rockford, IL). Briefly, 401 µl of S20 (about 6.0 mg/ml), 64 µl of Sulfo-NHS-  
 25 LC-Biotin (10 mg/ml), and 598 µl of kit PBS buffer is allowed to react on ice for 2 hours. Excess biotin is removed by column desalting, dialysis or both. Desalting is performed by adding the product to a 10 ml desalting column that had been equilibrated with 30 ml of PBS buffer. The one milliliter sample is allowed to permeate the gel and 1 ml fractions is collected. Fractions are monitored by the Bio

Rad Protein Assay (Bio Rad, Hercules, CA). Dialysis is performed using a Pierce Slide-A-Lyzer 10K cassette (Pierce, Rockford, IL), under constant stirring for 16 hours at 4°C against 2 liters of 30 mM Phosphate buffer (pH 7.0), 400 mM NaCl.

*Multiscreen Assay and Scintillation Proximity Assay (SPA)*

- 5 The binding assay reported by Vartikar (1989) is modified as follows: S20 was diluted into TK buffer (350 mM KCl, 10 mM  $\beta$ -mercaptoethanol, 30 mM Tris [pH 7.6]) and incubated at 37°C for 30 minutes. Labelled RNA is renatured in buffer (350 mM KCl, 20 mM MgSO<sub>4</sub>, 10 mM  $\beta$ -mercaptoethanol, 30 mM Tris [pH 7.6]) at 40°C for 20 minutes. After renaturation, the S20 (30  $\mu$ l) and 16S-rRNA (20  $\mu$ l) is incubated at
- 10 room temperature for 10 minutes. A Multiscreen HA opaque 96 well filtration plate (Millipore; Bedford, MA) is first prewetted with 100  $\mu$ l of Dulbecco's PBS for 10 minutes and vacuumed to remove excess fluid. The S20-16S-rRNA complex is transferred to the Multiscreen plate, incubated for 5 minutes, vacuumed, air dried for 1 hour, and counted with 40  $\mu$ l of scintillation cocktail on a Topcount™ Microplate
- 15 Scintillation Counter. The SPA assay is run almost identical to the Multiscreen assay except that it utilized biotinylated S20 and streptavidin coated SPA beads (Amersham) in the final reaction. As before the S20 and 16S-rRNA is allowed to react for 10 minutes. Fifty  $\mu$ l of SPA beads (20 mg/ml) is added to the 50  $\mu$ l of S20:16S-rRNA complex in a Dynatech Microlite plate and counted in a Topcount™ Microplate
- 20 Scintillation Counter. Inhibition studies are conducted with 16S/23S-rRNA and MS2-mRNA purchased from Roche Molecular Biochemicals, Indianapolis, IN. To identify potential inhibitors of the 16S RNA-20S complex the assay is run in the presence and absence of potential inhibitors and the effect on binding is assessed.

**Simultaneous assay of S4, S7, S8, S15, S17 and S20 binding to 16S RNA:**

- 25 While the discussion above, illustrates an assay useful for the identification of inhibitors which directly disrupt the interaction between the S20 polypeptide and the 16S ribosomal RNA. It is recognized that the binding of the S20 polypeptide may, in part, be dependent on the interaction of other direct binding S-proteins binding in concert to the 16S ribosomal RNA. Such dependence may be the result of alterations
- 30 in the conformation of the 16S ribosomal RNA or

In another embodiment, all the direct binding S-proteins can be incubated with 16S RNA and the presence of bound or unbound S20 polypeptide determined.

Indeed, the identity of all of the bound or unbound proteins can be determined. The

identity of a bound or unbound S protein can be determined, for instance by a suitable mass spectrometry technique, such as matrix-assisted laser desorption/ionization combined with time-of-flight mass analysis (MALDI-TOF MS) or electrospray ionization mass spectrometry (ESI MS). See Jensen et al., 1977, Protein Analysis By  
5 Mass Spectrometry, In Creighton (ed.), Protein Structure, A Practical Approach (Oxford University Press), Oxford, pp. 29-57; Patterson & Aebersold, 1995, Electrophoresis 16: 1791-1814; Figey et al., 1996, Analyt. Chem. 68: 1822-1828 (each of which is incorporated herein by reference in its entirety). Preferably, a separation technique such as HPLC or capillary electrophoresis is directly or indirectly  
10 coupled to the mass spectrometer. See Ducret et al., 1996, Electrophoresis 17: 866-876; Gevaert et al., 1996, Electrophoresis 17: 918-924; Clauser et al., 1995, Proc. Natl. Acad. Sci. USA 92: 5072-5076 (each of which is incorporated herein by reference in its entirety).

15

### Example 5

#### Assay of S20 with Other Direct Binding Proteins

This assay is used to test for direct RNA:protein assembly. The starting material proteins are preferably prepared by recombinant means and over-expression in a suitable host essentially as described in Examples 1, 2 and 3 for S20 with obvious  
20 modifications to reflect the differing sequences of the proteins involved. The nucleotide sequences of cDNA's encoding *S. aureus* direct binding ribosomal proteins S4, S7, S8, S15 and S17 are presented in SEQ ID NOS:11, 13, 15, 17 and 19 respectively. Sequences encoding S4, S7, S8, S15, and S17 can be isolated by means of the polymerase chain reaction. Primers are selected such that entire coding region  
25 is isolated. The complete amino acid sequences of S4, S7, S8, S15, and S17 polypeptides are presented in SEQ ID NOS:12, 14, 16, 18 and 20. Sequences encoding S4, S7, S8, S15, and S17 can be isolated by means of probing a genomic *Staphylococcus aureus* library with probes designed from SEQ ID NOS:11, 13, 15, 17 and 19 as well. The polymerase chain reaction would be a preferred method because  
30 it generally allows the isolation of a complete coding sequence in one experiment.

Methods for preparing and using probes and primers are described, for example, in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, ed. Sambrook et al., Cold Spring Harbor Laboratory Press, Cold Spring

Harbor, N.Y., 1989; Current Protocols in Molecular Biology, ed. Ausubel et al., Greene Publishing and Wiley-Interscience, New York, 1987 (with periodic updates); and Innis et al., PCR Protocols: A Guide to Methods and Applications, Academic Press: San Diego, 1990.

5           Primers are selected to have low self- or cross-complementarity, particularly at the 3' ends of the sequence. Long homopolymer tracts and high GC content are avoided to reduce spurious primer extension. Primers are typically about 20 residues in length, but this length can be modified as well-known in the art, in view of the particular sequence to be amplified. Computer programs are available to aid  
10 in these aspects of the design. One widely used computer program for designing PCR primers is (OLIGO 4.0 by National Biosciences, Inc., 3650 Annapolis Lane, Plymouth, Mich.). Another is Primer (Version 0.5,(c) 1991, Whitehead Institute for Biomedical Research, Cambridge, Mass.).

Isolated 16S RNA is prepared as described in Example 4.

15           In this assay all six of the S-proteins that bind directly to 16S RNA are added together with test compound. Unbound S-proteins are then removed by size-separation or filtration. Automated LC/ESI ion-trap or MALDI-tof-MS is then used to determine if a particular S-protein is inhibited in its binding to 16S RNA. Mass spectrometry is an ideal detection tool since all of the S-protein average masses are  
20 known and unique. An example illustrates how specific inhibition of S20 protein binding to RNA is detected. The concept is illustrated in Figure 4.

RNA:protein assembly is assayed in 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>, 330 mM NaCl at 42 °C. The procedure is based on the conditions of Culver and Noller (RNA, 1999, 5: 832-843) except that 0.01% Nikkol detergent is removed  
25 because it significantly complicates the LC/MS analysis. Primary ribosomal binding proteins S4, S7, S8, S15, S17, and S20 are dialyzed overnight against 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>, 1 M NaCl. In the reconstitution, 200 pmol *in vitro* transcribed 16S RNA is incubated at 42 °C for 15 minutes. Then, 800 pmol S7, S8, S15, S17, and S4 each are added to the RNA, followed by 400 pmol S20. The NaCl  
30 concentration is then adjusted to 330 mM by adding 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>. The mixture is then incubated at 42 °C for 20 more minutes. The protein:RNA complex is then separated from the free proteins by spinning in a YM-100 Microcon at 500 xg for 20 minutes. The RNA is precipitated from the retentate



by adding 2 volumes of acetic acid and incubating on ice for 45 minutes. Proteins from both the flow-through and retentate are analyzed by LC/ESI ion trap mass spectrometry. The proteins are first separated on a C4 reversed phase column (Vydac) using a gradient from 98% of 0.1% TFA, 2% of 90% acetonitrile/0.1% TFA to 100% of 90% acetonitrile/0.1 % TFA. The intact mass of each protein are observed by  
5 electrospray mass spectrometry as it eluted from the column.

We have also been able to identify S20 in a mixture of primary ribosomal binding proteins by MALDI-TOF mass spectrometry. The mixture of proteins is passed over a C18 zip-tip (Millipore) to remove salts, eluting in 80%  
10 acetonitrile/0.1% TFA. A saturated solution of sinapinic acid is prepared in 30% acetonitrile/0.1% TFA. One microliter of the protein solution is mixed with ten microliters of the matrix solution, and 0.5 uL is spotted onto the stainless steel MALDI target. MALDI-TOF data were collected in linear mode from 6000-25000 Da, and the intact mass for S20 is observed.

15 Of course, purified direct binding proteins make possible assays to access the association of any or all direct binding proteins with 16S RNA. The invention of course, includes methods for testing for inhibitors of ribosomal assembly in which the incorporation of any direct binding protein into the polyribonucleotide protein complex is accessed.

20

### Example 6

#### Scintillation Proximity Assay (SPA)

##### Assay of S20 with Other Direct Binding Proteins

As in the previous example all S4, S7, S8, S15 and S17 are incubated together with 16S RNA followed by S20 ribosomal polypeptide in the presence and absence of  
25 a test compound. Starting materials are prepared roughly as described in previous examples. In this example the 16S ribosomal RNA is end labeled with biotin and the S20 ribosomal polypeptide is radioactively labeled.

Primary ribosomal binding proteins S4, S7, S8, S15, S17, and S20 are dialyzed overnight against 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>, 1 M NaCl. In the  
30 reconstitution, 200 pmol *in vitro* transcribed 16S RNA is incubated at 42 °C for 15 minutes. Then, 800 pmol S7, S8, S15, S17, and S4 each are added to the RNA, followed by 400 pmol S20. The NaCl concentration is then adjusted to 330 mM by adding 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>. Fifty µl streptavidin coated SPA

beads (20 mg/ml) is added to the 50 µl of the reaction mixture in a Dynatech Microlite plate and counted in a Topcount<sup>TM</sup> Microplate Scintillation Counter. To identify potential inhibitors of S20 incorporation into the polyribonucleotideprotein complex, the assay is run in the presence and absence of potential inhibitors and the effect on binding is assessed.

#### **Protein-protein Interaction Assembly Screen**

The isolated S20 polypeptide of the invention also makes possible an assay through which one may detect all possible protein-protein disruptions in the 30S assembly process. This is important since published assembly maps are not based on the myriad of possible protein-protein interactions that may occur. In practice these maps are based on limited S-protein combinations that were tested *in vitro*. This assay makes use of the fact that the assembly of ribosomes in general and the 30S subunit in particular, is an ordered process and makes use of all 21 small subunit ribosomal proteins or a limited subset of those proteins. The S3 ribosomal protein is known to integrate itself last or very late in the ribosomal assembly process. Its efficient integration is known to be dependent upon the proper integration of the direct binding ribosomal proteins as well non-direct binding proteins. Proper partial assembly is monitored by measuring the incorporation of S3 ribosomal polypeptide into the partially or fully assembled ribosome. In the alternative, improper or disrupted assembly can be assayed by exclusion of S3 ribosomal polypeptide from the ribosome

The S3 ribosomal protein may be labeled as discussed hereinbefore for ease of detection. The 16S ribosomal RNA or a direct binding ribosomal peptide may be immobilized or the entire assay may be performed with all components in solution phase. The starting materials for the assays are preferably prepared by recombinant means. The DNA sequences encoding all 21 30S subunit proteins are provided in the sequence listings as well as the amino acids sequences encoded by each. The invention provides ribosomal assembly assays utilizing all 21 small subunit ribosomal proteins as well as a select subset of proteins readily apparent to one skilled in the art. Sequences encoding each protein can be isolated by means of the polymerase chain reaction. Primers are selected as discussed previously. Primers are selected as discussed previously. Primers are selected such that entire coding region is isolated. Methods for preparing and using probes and primers are discussed above.

Exemplary forward and reverse primers suitable for amplification of S4, S6, and S18 are described listed here by way of example. One skilled in the art would recognize that other primers may be equally suitable.

S4 Forward 5'-TATATTATCGATAATGGCTCGATTCAGAGGT-3' (SEQ ID

5 NO:53)

S4 Reverse 5'-TATAGGATCCTTAACGGATTAATTGTTTCGTTAATTT-3' (SEQ ID NO:54)

S18 Forward 5'-TATATTATCGATAATGGCAGGTGGACCAAGAAG-3' (SEQ ID NO:55)

10 S18 Reverse 5'-TATAGGATCCTTATTGTTCTTCTTTAACAT-3' (SEQ ID NO:56)

S6 Forward 5'-TATATTATCGATAATGAAGAAACATATGAAGTTAT-3' (SEQ ID NO:57)

S6 Reverse 5'-TATAGGATCCTTACTTGTCTTCGTCTTCAC-3' (SEQ ID NO:58)

The following is provided by way of non-limiting example.

15

#### **Example 7**

##### **Partial Ribosomal Assembly Assay**

In this assay format several S-proteins are allowed to interact with 16S RNA in the presence of a test compound (Fig.5). The assay makes use of all of the direct binding ribosomal proteins except S15 (S4, S7, S8, S17 and S20) and a select group of *S. aureus* ribosomal proteins which integrate themselves into the ribosome by reliance on protein-protein or protein-RNA interactions (S3, S5, S9, S10, S12, S14, S16 and S19)

The starting material proteins are prepared by recombinant means and over-expression in a suitable host essentially as described in Examples 1, 2 and 3 for the S20 polypeptide of the invention with obvious modifications to reflect the differing sequences of the proteins involved. The nucleotide sequences of cDNA's encoding *S. aureus* direct binding ribosomal proteins S4, S7, S8, and S17 are presented in SEQ ID NOS:11, 13, 15, and 19 respectively. The production of the isolated S20 polypeptide of the invention is described hereinbefore.

30 The nucleotide sequences of cDNA's encoding *S. aureus* ribosomal proteins which integrate themselves into the ribosome by reliance on protein-protein or protein-RNA interactions (non-direct binding ribosomal proteins) S3, S5, S9, S10, S12, S14, S16 and S19 are presented in SEQ ID NOS: 26, 28, 32, 34, 38, 42, 44, and

48 respectively. Nucleotide sequences encoding *S. aureus* S3, S4, S5, S7, S8, S9, S10, S12, S14, S16 S17 and S19 can be isolated by means of the polymerase chain reaction. Primers are selected such that the entire amino acid coding region is isolated. The complete amino acid sequences of *S. aureus* S3, S4, S5, S7, S8, S9, S10, S12, S14, S16 S17 and S19 polypeptides are presented in SEQ ID NOS:27, 12, 29, 14, 16, 33, 35, 39, 43, 45, 20 and 49. Sequences encoding S3, S4, S5, S7, S8, S9, S10, S12, S14, S16 S17 and S19 can be isolated by means of probing a genomic *Staphylococcus aureus* library with probes designed from SEQ ID NOS:12, 28, 13, 15, 32, 34, 38, 42, 44, 19, and 48 as well. The polymerase chain reaction would be a preferred method because it generally allows the isolation of a complete coding sequence in one experiment. The S3 protein is labeled, preferably radiolabeled.

RNA:protein assembly is assayed in 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>, 330 mM NaCl at 42 °C. The procedure is based on the conditions of Culver and Noller (RNA, 1999, 5: 832-843) except that 0.01% Nikkol detergent is removed because it significantly complicates the LC/MS analysis. Ribosomal proteins S3, S4, S5, S7, S8, S9, S10, S12, S14, S16, S17, S19 and S20 are dialyzed overnight against 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>, 1 M NaCl. In the reconstitution, 200 pmol *in vitro* transcribed 16S RNA is incubated at 42 °C for 15 minutes. Then, 800 pmol ribosomal proteins S4, S7, S8, S17, and S20 added to the RNA, followed by ribosomal proteins, S5, S9, S10, S12, S14, S16 and S19. The NaCl concentration is then adjusted to 330 mM by adding 80 mM K<sup>+</sup>-HEPES, pH 7.6, 20 mM MgCl<sub>2</sub>. The mixture is then incubated at 42 °C for 20 more minutes. 800 pmol labeled ribosomal protein S3 is then added.

Unbound S-proteins are removed by size-separation or filtration. If the labelled S3 protein is present in the RNA:multi-protein complex then the compound does not inhibit any specific protein-protein interactions during the assembly process. If the compound prevents the incorporation of labelled S3 protein then the assay reveals that the test compound inhibits a protein-protein interaction.

The partially assembled RNA:multi-protein complex is then analyzed by LC/ion-trap electrospray analysis to determine the S-protein components in the partially assembled complex. Alternatively MALDI-tof-MS can be used. Knowing the identity of S-proteins in the partially assembled complex and published knowledge of how the 30S subunit is assembled *in vitro* (Noller and Nomura (1987) the protein-

protein interaction that is disrupted by the test compound may be determined. The exact protein-protein interaction that is disrupted can be determined using selective combinations of S-proteins added to 16S RNA and compound. As stated above, this is an important confirmation process since published *in vitro* assembly maps are based on a limited data set. Assembly disruption by the test compound can be independently verified by analytical ultracentrifugation analysis (Fig.6). In this process the partially assembled 30S complex is differentiated from intact complex by displaying a lower rate of sedimentation in a given centrifugal field (i.e., as measured by a lower sedimentation constant, expressed in Svedberg units or S). The contents of sedimentation clusters can be verified by mass spectrometry.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the invention.

The entire disclosure of all publications cited herein are hereby incorporated by reference.

**CLAIMS**

What is claimed is:

1. An isolated nucleic acid comprising a nucleotide sequence that encodes an amino  
5 acid sequence having at least 85% identity with SEQ ID NO:2
2. An isolated nucleic acid comprising the nucleotide sequence having least 85%  
identity with SEQ ID NO:1
- 10 3. An isolated nucleic acid comprising a nucleotide sequence that encodes the amino  
acid sequence of SEQ ID NO:2
4. An isolated nucleic acid comprising the nucleotide sequence of SEQ ID NO:1
- 15 5. An isolated nucleic acid comprising a nucleotide sequence that encodes the amino  
acid sequence having at least 85% identity with residues 10 through 83 of SEQ ID  
NO:2
6. An isolated nucleic acid comprising the nucleotide sequence having least 85%  
20 identity with nucleotides 28 through 249 of SEQ ID NO:1
7. An isolated nucleic acid comprising a nucleotide sequence that encodes the amino  
acid sequence residues 10 through 83 of SEQ ID NO:2
- 25 8. An isolated nucleic acid comprising nucleotides 28 through 249 of SEQ ID NO:1
9. An isolated S20 ribosomal polypeptide comprising an amino acid sequence having  
least 85% identity to the sequence of SEQ ID NO:2.
- 30 10. An isolated S20 ribosomal polypeptide comprising the amino acid sequence of  
SEQ ID NO:2.

11. An isolated S20 ribosomal polypeptide comprising an amino acid sequence having  
least 85% identity to residues 10 through 83 of SEQ ID NO:2.
12. An isolated S20 ribosomal polypeptide comprising residues 10 through 83 of SEQ  
5 ID NO:2
13. The isolated S20 ribosomal polypeptide of claim 11 which comprises a label.
14. The isolated S20 ribosomal polypeptide of claim 11 wherein the label is selected  
10 from the group consisting of: radiolabels, fluorescent labels, amino acid tags and  
biotin.
15. The isolated S20 ribosomal polypeptide of claim 13 wherein said S20 ribosomal  
polypeptide comprises a radiolabel.
- 15 16. The isolated S20 ribosomal polypeptide of claim 13 wherein said S20 ribosomal  
polypeptide comprises a fluorescent label.
17. The isolated S20 ribosomal polypeptide of claim 13 wherein said S20 ribosomal  
20 polypeptide comprises an amino acid tag.
18. The isolated S20 ribosomal polypeptide of claim 13 wherein said S20 ribosomal  
polypeptide comprises a biotin molecule
- 25 19. A vector comprising the nucleic acid of claim 5
20. A host cell comprising the vector of claim 19
21. A method of making isolated an S20 ribosomal polypeptide comprising:  
30 a) introducing the nucleic acid of claim 5 into a host cell  
b) maintaining said host cell under conditions whereby said nucleic acid is  
expressed to produce said S20 ribosomal polypeptide  
c) purifying said S20 ribosomal polypeptide

22. A method for testing for inhibitors of ribosomal assembly comprising the steps of:
- a) contacting the S20 ribosomal polypeptide of claim 11 with a 16S ribosomal RNA
    - i 5 (i) in the presence of a test agent; and
    - (ii) in the absence of said test agent; and
  - b) determining the amount of said S20 ribosomal polypeptide specifically bound to said RNA
    - (i) in the presence of a test agent; and
    - 10 (ii) in the absence of said test agent; and
  - c) comparing the amount of said S20 ribosomal polypeptide determined in step (b)(i) to the amount of said S20 ribosomal polypeptide determined in step (b)(ii);
23. The method of claim 22 wherein said S20 ribosomal polypeptide comprises  
15 residues 10 through 83 of SEQ ID NO:2
24. The method of claim 22 wherein said S20 ribosomal polypeptide is labeled
25. The method of claim 22 wherein said S20 ribosomal polypeptide comprises a  
20 radiolabel
26. The method of claim 22 wherein said S20 ribosomal polypeptide comprises an amino acid tag.
- 25 27. The method of claim 22 wherein said S20 ribosomal polypeptide comprises a biotin molecule.
28. The method of claim 22 wherein said 16S ribosomal RNA comprises nucleotide position 1419 to 1502 of SEQ ID NO:21.  
30
29. The method of claim 22 wherein said 16S ribosomal RNA comprises nucleotide position 120 to 322 of SEQ ID NO:21.



30. The method of claim 22 wherein said 16S ribosomal RNA is labeled
31. The method of claim 22 wherein said 16S ribosomal RNA comprises a radiolabel
- 5 32. The method of claim 22 wherein said 16S ribosomal RNA comprises a biotin molecule
33. The method of claim 22 wherein said S20 ribosomal polypeptide is attached to a solid support.
- 10 34. The method of claim 22 wherein said 16S ribosomal RNA is attached to a solid support
35. A method for testing for inhibitors of ribosomal assembly comprising the steps of:
- 15 Contacting at least one direct binding ribosomal polypeptide selected from the group consisting of S4, S7, S8, S15, S17 and S20 with 16S ribosomal RNA
- (i) in the presence of a test agent; and
  - (ii) in the absence of said test agent; and
- b) determining the amount of direct binding protein bound to the RNA
- 20 (i) in the presence of a test agent; and
- (ii) in the absence of said test agent; and
- c) comparing the amount direct binding protein determined in step (b)(i) to the amount of direct binding protein determined in step (b)(ii);
- 25 36. The method of claim 35 wherein the direct binding ribosomal proteins comprise S4, S7, S8 and S20.
37. The method of claim 35 wherein the direct binding ribosomal proteins comprise S4, S7, S8, S17 and S20
- 30 38. The method of claim 35 wherein the direct binding ribosomal proteins comprise S4, S7, S8, S17, S15 and S20.

39. The method of claim 35 wherein said direct binding ribosomal polypeptide is labeled
40. The method of claim 35 wherein said direct binding ribosomal polypeptide  
5 comprises a radiolabel
41. The method of claim 35 wherein said direct binding ribosomal polypeptide comprises an amino acid tag.
- 10 42. The method of claim 35 wherein said direct binding ribosomal polypeptide comprises a biotin molecule
43. The method of claim 35 wherein said 16S ribosomal RNA is labeled
- 15 44. The method of claim 35 wherein said 16S ribosomal RNA comprises a radiolabel
45. The method of claim 35 wherein said 16S ribosomal RNA comprises a biotin molecule
- 20 46. The method of claim 35 wherein said direct binding ribosomal polypeptide is attached to a solid support.
47. The method of claim 35 wherein said 16S ribosomal RNA is attached to a solid support
- 25 48. A method for testing for inhibitors of ribosomal assembly comprising the steps of:
- a) contacting S20 ribosomal polypeptide and at least one other direct binding ribosomal polypeptide selected from the group consisting of S4, S7, S8, S15  
30 and S17 with 16S ribosomal RNA in the
- (i) in the presence of a test agent; and
- (ii) in the absence of said test agent; and

- b) determining the amount of S20 ribosomal polypeptide or any other direct binding protein bound to the RNA
- (i) in the presence of a test agent; and
  - (ii) in the absence of said test agent; and
- 5 c) comparing the amount of S20 ribosomal polypeptide or any other direct binding protein determined in step (b)(i) to the amount of S20 ribosomal polypeptide or any other direct binding protein determined in step (b)(ii);
49. The method of claim 48 wherein the other direct binding ribosomal proteins
- 10 comprise S4, S7, S8.
50. The method of claim 48 wherein the other direct binding ribosomal proteins comprise S4, S7, S8 and S17.
- 15 51. The method of claim 48 wherein the other direct binding ribosomal proteins comprise S4, S7, S8, S17, S15.
52. The method of claim 48 wherein said S20 ribosomal polypeptide or other direct binding ribosomal polypeptide is labeled
- 20 53. The method of claim 48 wherein said S20 ribosomal polypeptide or other direct binding ribosomal polypeptide comprises a radiolabel
54. The method of claim 48 wherein said S20 ribosomal polypeptide or other direct binding ribosomal polypeptide comprises an amino acid tag.
- 25 55. The method of claim 48 wherein said S20 ribosomal polypeptide or other direct binding ribosomal polypeptide comprises a biotin molecule
- 30 56. The method of claim 48 wherein said 16S ribosomal RNA is labeled
57. The method of claim 48 wherein said 16S ribosomal RNA comprises a radiolabel

58. The method of claim 48 wherein said 16S ribosomal RNA comprises a biotin molecule
59. The method of claim 48 wherein said S20 ribosomal polypeptide or other direct  
5 binding ribosomal polypeptide is attached to a solid support.
60. The method of claim 48 wherein said 16S ribosomal RNA is attached to a solid support
- 10 61. A method for testing for inhibitors of ribosomal assembly comprising the steps of:
- a.) contacting at least one direct binding ribosomal polypeptide selected from the group consisting of S4, S7, S8, S15, S17 and S20 with 16S ribosomal RNA to form a polyribonucleotide protein complex and;
  - b) contacting said polyribonucleotide protein complex with at least one non-  
15 direct binding ribosomal polypeptide selected from the group consisting of S1, S2, S3, S5, S6, S9, S10, S11, S12, S13, S14, S16, S18, S19, and S21.
    - (i) in the presence of a test agent; and
    - (ii) in the absence of said test agent; and
  - c) determining the amount of at least one non- direct binding ribosomal  
20 polypeptide bound to the RNA
    - (i) in the presence of a test agent; and
    - (ii) in the absence of said test agent; and
  - d.) comparing the amount of least one non direct binding ribosomal polypeptide  
25 determined in step (c)(i) to the amount of non-direct binding ribosomal polypeptide protein determined in step (c)(ii);
62. The method of claim 61 wherein the direct binding ribosomal proteins comprise S4, S7, S8.
- 30 63. The method of claim 61 wherein the direct binding ribosomal proteins comprise S4, S7, S8 and S17.

64. The method of claim 61 wherein the direct binding ribosomal proteins comprise S4, S7, S8, S17, S15.
- 5 65. The method of claim 61 wherein the direct binding ribosomal proteins comprise S4, S7, S8, S17, S15 and S20
66. The method of claim 61 wherein the non-direct binding ribosomal proteins comprise S16
67. The method of claim 61 wherein the non-direct binding ribosomal proteins  
10 comprise S3, S5, S9, S10, S12, S14, S16 and S19
68. The method of claim 61 wherein said direct binding or non-direct binding ribosomal polypeptide is labeled
- 15 69. The method of claim 61 wherein said direct binding or non-direct binding ribosomal polypeptide comprises a radiolabel
70. The method of claim 61 wherein said direct binding or non-direct binding ribosomal polypeptide comprises an amino acid tag.  
20
71. The method of claim 61 wherein said direct binding or non-direct binding ribosomal polypeptide comprises a biotin molecule
72. The method of claim 61 wherein said 16S ribosomal RNA is labeled  
25
73. The method of claim 61 wherein said 16S ribosomal RNA comprises a radiolabel
74. The method of claim 61 wherein said 16S ribosomal RNA comprises a biotin molecule  
30
75. The method of claim 61 wherein said direct binding or non-direct binding ribosomal polypeptide is attached to a solid support.

76. The method of claim 61 wherein said 16S ribosomal RNA is attached to a solid support

77. A method for testing for inhibitors of ribosomal assembly comprising the steps of:

- 5 a.) contacting S4, S7, S8, S17 and S20 ribosomal polypeptides with 16S ribosomal RNA to form a polyribonucleotide protein complex and;
- b) contacting said polyribonucleotide protein complex with non- direct binding ribosomal polypeptides S3, S5, S9, S10, S12, S14, S16 and S19 to form a resultant polyribonucleotide protein complex
- 10 (iii) in the presence of a test agent; and
- (iv) in the absence of said test agent; and
- d) contacting non-direct binding ribosomal polypeptide S3 with said resultant polyribonucleotide protein complex;
- and determining the amount of said non-direct binding ribosomal polypeptide S3
- 15 bound to said resultant polyribonucleotide protein complex;
- (i) formed in the presence of said test agent; and
- (ii) formed in the absence of said test agent; and
- e) comparing the amount of S3 determined in step (d)(i) to the amount of S3 determined in step (d)(ii)
- 20 78. The method of claim 77 wherein said non-direct binding ribosomal polypeptide S3 is labeled.
79. The method of claim 78 wherein said non-direct binding ribosomal polypeptide S3 is radiolabeled

*Figure 1*

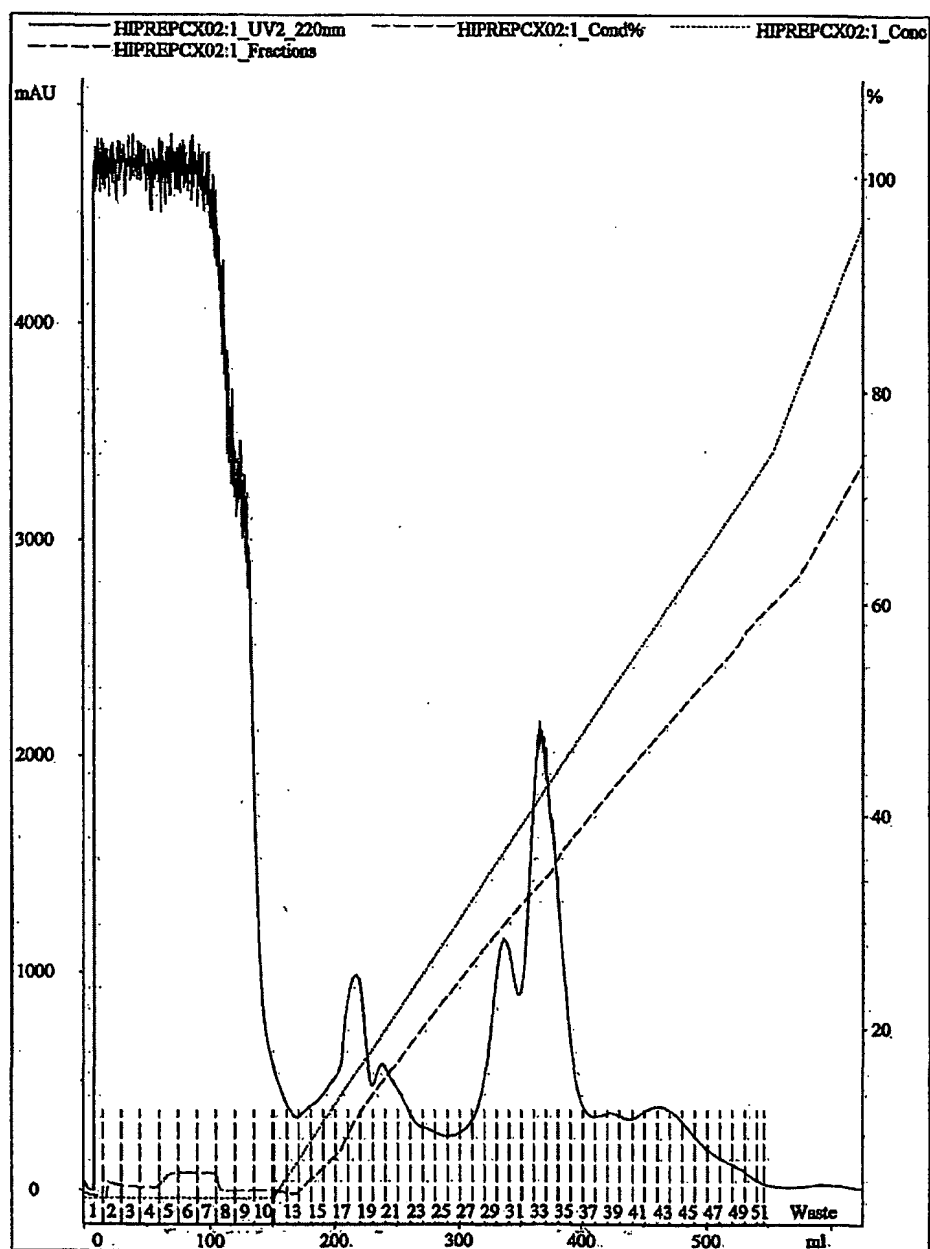
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*Figure 2*



**Figure 3**

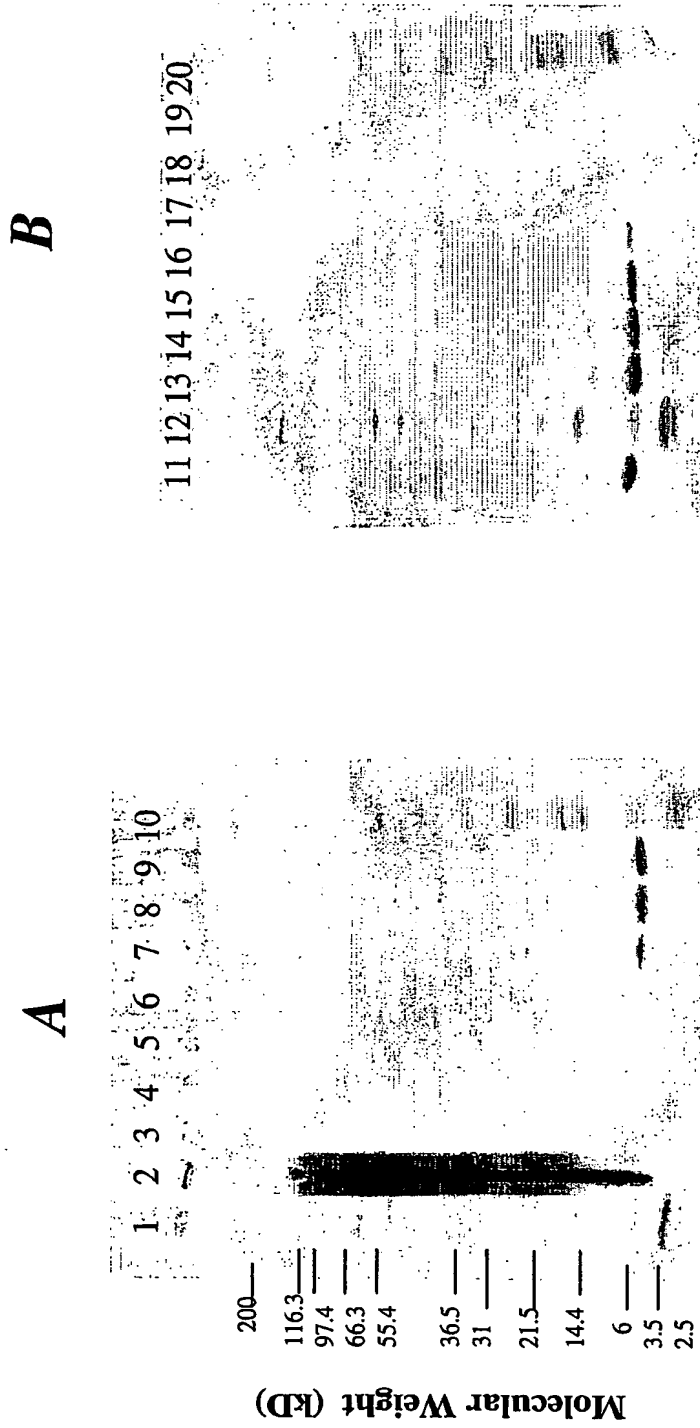
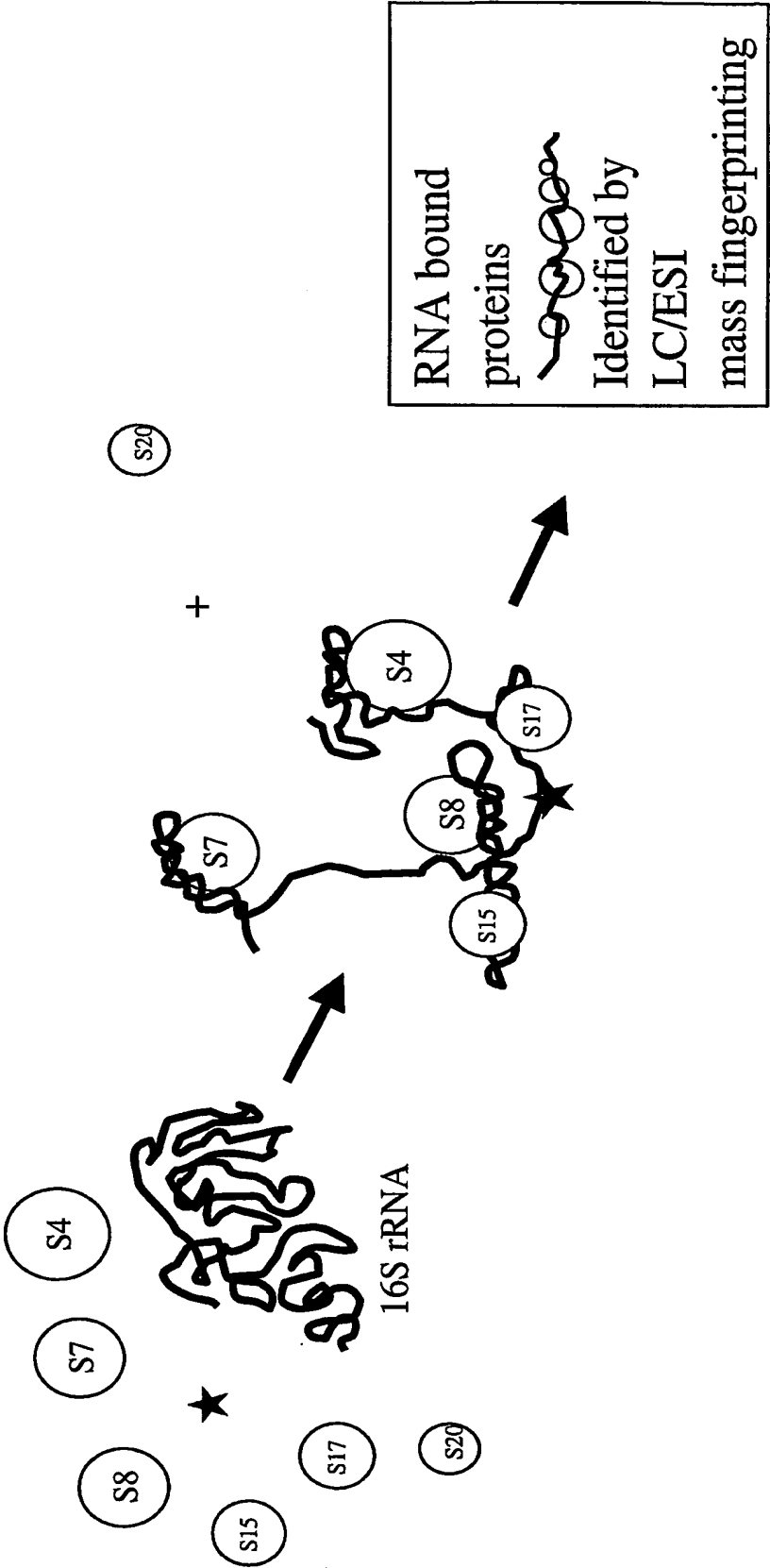
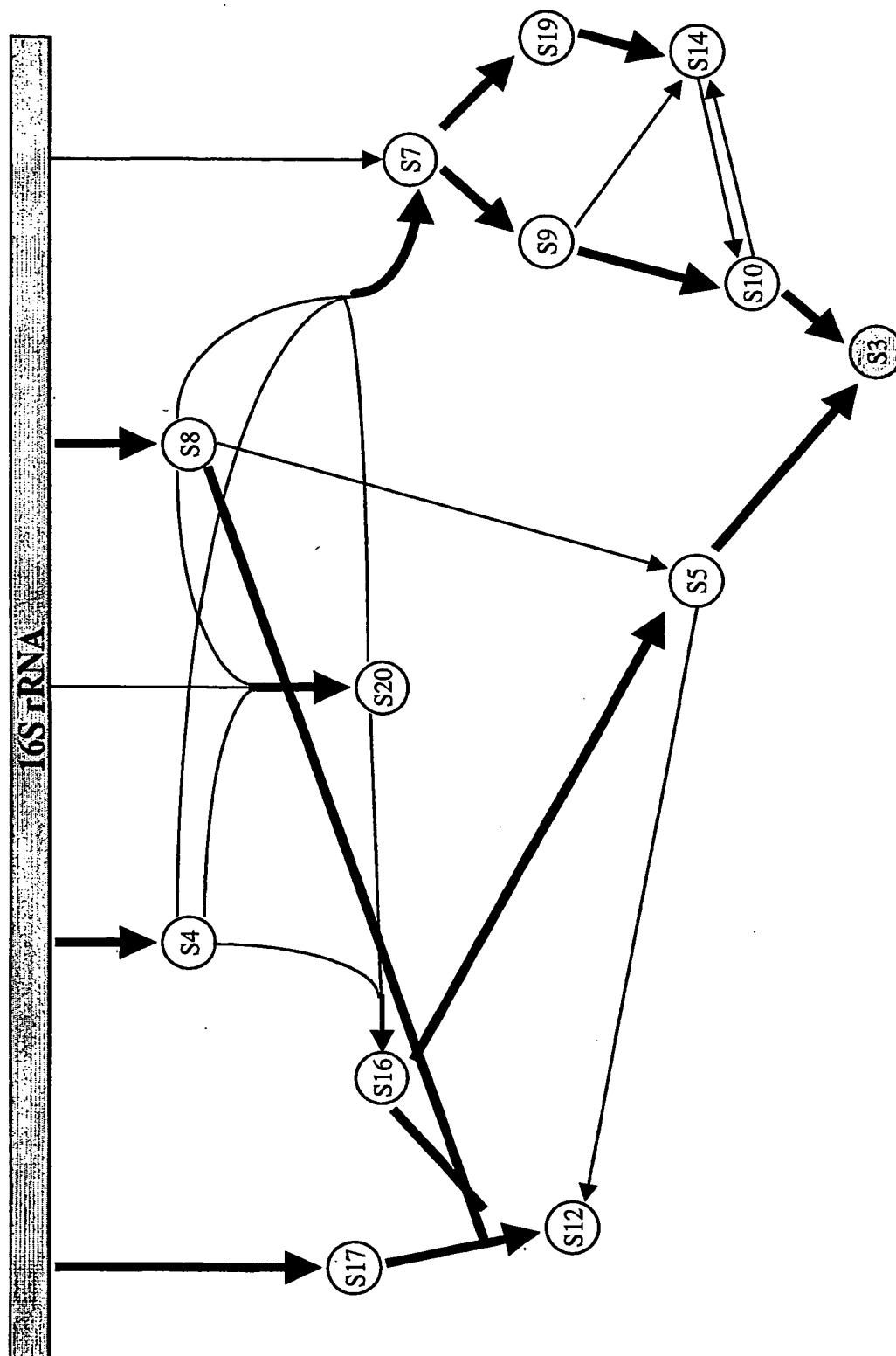
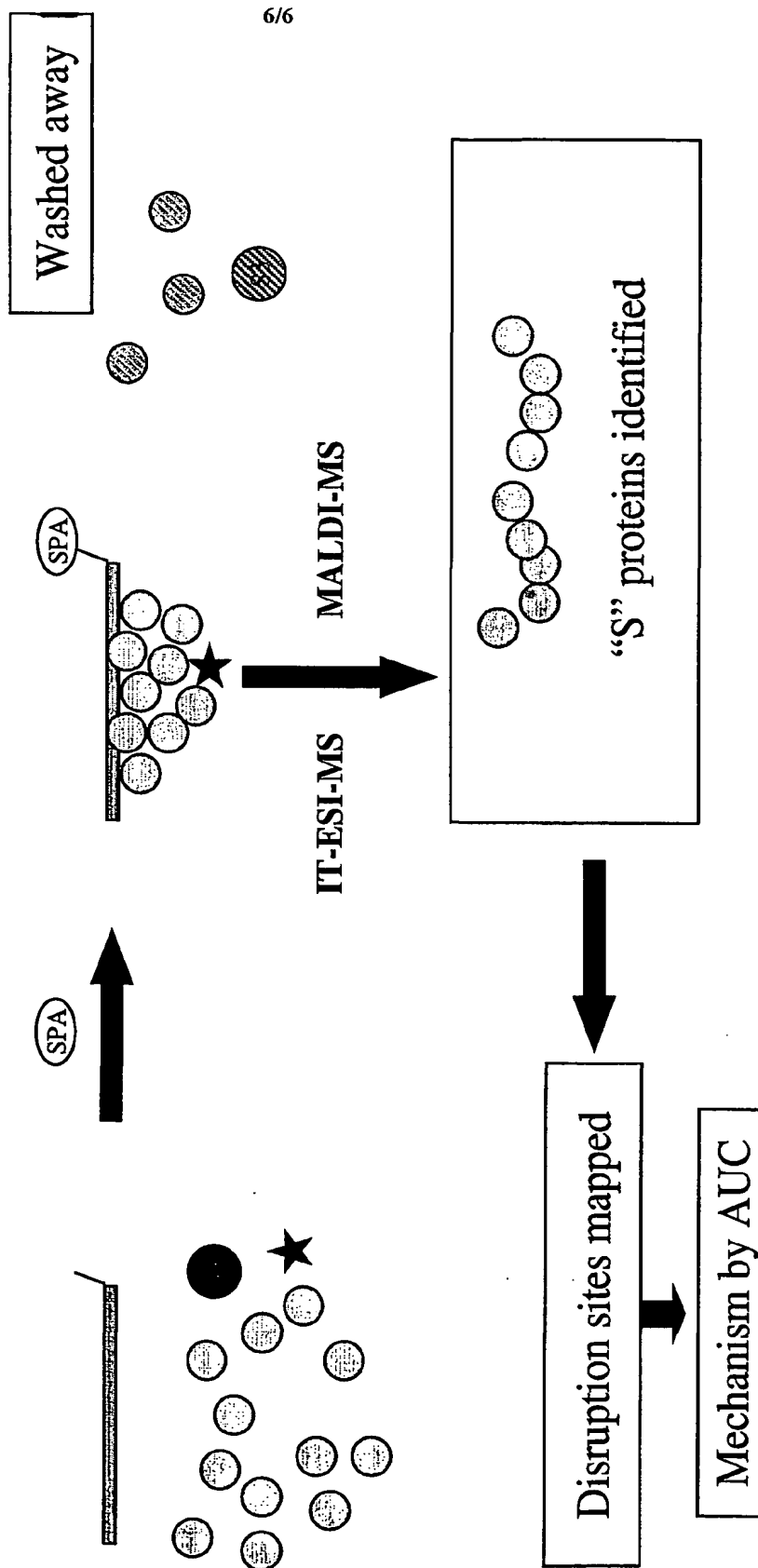


Figure 4



*Figure 5*

*Figure 6*

## SEQUENCE LISTING

<110> Pearson, James D  
Slightom, Jerry  
Chosay, John G.  
McCroskey, Mark C.  
Shinabarger, Dean L.  
Wilcox, Sheri

<120> Complete Nucleotide Sequence of Staphylococcus aureus  
Ribosomal Protein Gene, S20 and Methods for the  
Identification of Antibacterial Substances

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35 40 45  
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 35           40           45

Leu Gln Leu Arg Glu Lys Gln Lys Leu Arg Tyr Leu Tyr Gly Met Thr
 50           55           60

Glu Arg Gln Phe Arg Asn Thr Phe Asp Ile Ala Gly Lys Lys Phe Gly
 65           70           75           80

Val His Gly Glu Asn Phe Met Ile Leu Leu Ala Ser Arg Leu Asp Ala
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Val Val Tyr Ser Leu Gly Leu Ala Arg Thr Arg Arg Gln Ala Arg Gln
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Leu Val Asn His Gly His Ile Leu Val Asp Gly Lys Arg Val Asp Ile
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tattaatgaa ttttcattaa gcgttcatgc ttagggcatc gccatatcta tcgtatttat 660
tcagtaa                                           667

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&lt;210&gt; 14



&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 14

Met Pro Arg Lys Gly Ser Val Pro Lys Arg Asp Val Leu Pro Asp Pro  
 1 5 10 15

Ile His Asn Ser Lys Leu Val Thr Lys Leu Ile Asn Lys Ile Met Leu  
 20 25 30

Asp Gly Lys Arg Gly Thr Ala Gln Arg Ile Leu Tyr Ser Ala Phe Asp  
 35 40 45

Leu Val Glu Gln Arg Ser Gly Arg Asp Ala Leu Glu Val Phe Glu Glu  
 50 55 60

Ala Ile Asn Asn Ile Met Pro Val Leu Glu Val Lys Ala Arg Arg Val  
 65 70 75 80

Gly Gly Ser Asn Tyr Gln Val Pro Val Glu Val Arg Pro Glu Arg Arg  
 85 90 95

Thr Thr Leu Gly Leu Arg Trp Leu Val Asn Tyr Ala Arg Leu Arg Gly  
 100 105 110

Glu Lys Thr Met Glu Asp Arg Leu Ala Asn Glu Ile Leu Asp Ala Ala  
 115 120 125

Asn Asn Thr Gly Gly Ala Val Lys Lys Arg Glu Asp Thr His Lys Met  
 130 135 140

Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp  
 145 150 155

&lt;210&gt; 15

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 15

atcgtaaatt taaattatgc cgtatttgtt tccgtgaatt agcttacaaa ggccaaatcc 60  
 ctggcggttcg taaagctagc tggtaataaa aaagagtcctg aaaggaggca acaatcaatg 120  
 acaatgacag atccaatcgc agatatgctt actcgtgttaa gaaacgcaaa catggtgcgt 180  
 cacgagaagt tagaattacc tgcatacaat attaaaaaag aaattgctga aatcttaaag 240  
 agtgaagggtt tcattaaaaa tgttgaatac gtagaagatg ataaacaagg tgtacttcgt 300  
 ttattcttaa aatatgggtca aaacgatgag cgtgttatca caggattaaa acgtatttca 360  
 aaaccagggtt tacgtgttta tgcaaaagct agcgaaatgc cttaaagtatt aaatgggttta 420  
 ggtattgcat tagtatcaac ttctgaagggt gtaatcactg acaaagaagc aagaaaacgt 480  
 aatgtttggtg gagaaattat cgcatacgtt tggtataaaa aaataaggag gtgccataac 540  
 atgagtcgtg ttggtaagaa aattattgac atccctagtg acgtaacagt aacttttgat 600  
 ggaaatcatg taact 615

&lt;210&gt; 16

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 16

Met Thr Met Thr Asp Pro Ile Ala Asp Met Leu Thr Arg Val Arg Asn

1                      5                      10                      15  
 Ala Asn Met Val Arg His Glu Lys Leu Glu Leu Pro Ala Ser Asn Ile  
                          20                                      25                                      30  
 Lys Lys Glu Ile Ala Glu Ile Leu Lys Ser Glu Gly Phe Ile Lys Asn  
                          35                                      40                                      45  
 Val Glu Tyr Val Glu Asp Asp Lys Gln Gly Val Leu Arg Leu Phe Leu  
                          50                                      55                                      60  
 Lys Tyr Gly Gln Asn Asp Glu Arg Val Ile Thr Gly Leu Lys Arg Ile  
                          65                                      70                                      75                                      80  
 Ser Lys Pro Gly Leu Arg Val Tyr Ala Lys Ala Ser Glu Met Pro Lys  
    85                                      90                                      95  
 Val Leu Asn Gly Leu Gly Ile Ala Leu Val Ser Thr Ser Glu Gly Val  
    100                                      105                                      110  
 Ile Thr Asp Lys Glu Ala Arg Lys Arg Asn Val Gly Gly Glu Ile Ile  
    115                                      120                                      125  
 Ala Tyr Val Trp  
    130

<210> 17  
 <211> 517  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 17  
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 gaacgtaaaa acgaaatcat taaagaatac cgtgtacacg aaactgatac tgggtcacca 180  
 gaagtacaaa tcgctgtact tactgcagaa atcaacgcag taaacgaaca cttacgtaca 240  
 cacaaaaaag accaccattc acgtcgtgga ttattaaaaa tggtaggtcg tcgtagacat 300  
 ttattaaact acttacgtag taaagatatt caacggtacc gtgaattaat taaatcactt 360  
 ggtatccgtc gttaatctta atataacgctc tttgagggtg gggcatatgt atgttccaac 420  
 cttaatttat attaaaaaag cttttttacaa atattaacat ttatttatatg ttaagcta 480  
 attgagtga taataaggtt acaatgagat aaagatg 517

<210> 18  
 <211> 89  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 18  
 Met Ala Ile Ser Gln Glu Arg Lys Asn Glu Ile Ile Lys Glu Tyr Arg  
                          1                                      5                                      10                                      15  
 Val His Glu Thr Asp Thr Gly Ser Pro Glu Val Gln Ile Ala Val Leu  
    20                                      25                                      30  
 Thr Ala Glu Ile Asn Ala Val Asn Glu His Leu Arg Thr His Lys Lys  
    35                                      40                                      45  
 Asp His His Ser Arg Arg Gly Leu Leu Lys Met Val Gly Arg Arg Arg  
    50                                      55                                      60

His Leu Leu Asn Tyr Leu Arg Ser Lys Asp Ile Gln Arg Tyr Arg Glu  
 65 70 75 80

Leu Ile Lys Ser Leu Gly Ile Arg Arg  
 85

<210> 19  
 <211> 401  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 19  
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 taagaggagg ttacaaaagt gagcgaaaga aacgatcgta aagtttatgt aggtaaagtt 120  
 gtttcagaca aaatggacaa gactattaca gtacttggtg aaacttacaa aacacacaaa 180  
 ttatacggta aacgagtaaa atactctaaa aaatacaaaa ctcattgatga aaacaattca 240  
 gctaaattag gagacattgt taaaattcaa gaaactcgtc ctttatcagc aacaaaacgt 300  
 ttctggtttg tagagattgt tgaagagtca gtaattattt aatacaagtt tagagataag 360  
 ggagggtttta ctaatgatcc aacaagaaac acgcttgaaa g 401

<210> 20  
 <211> 87  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 20  
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 1 5 10 15  
 Asp Lys Met Asp Lys Thr Ile Thr Val Leu Val Glu Thr Tyr Lys Thr  
 20 25 30  
 His Lys Leu Tyr Gly Lys Arg Val Lys Tyr Ser Lys Lys Tyr Lys Thr  
 35 40 45  
 His Asp Glu Asn Asn Ser Ala Lys Leu Gly Asp Ile Val Lys Ile Gln  
 50 55 60  
 Glu Thr Arg Pro Leu Ser Ala Thr Lys Arg Phe Arg Leu Val Glu Ile  
 65 70 75 80  
 Val Glu Glu Ser Val Ile Ile  
 85

<210> 21  
 <211> 1555  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 21  
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 acgtggataa cctacctata agactgggat aacttcggga aaccggagct aataccggat 180  
 aatattttga accgcatggg tcaaaagtga aagacggtct tgctgtcact tatagatgga 240  
 tccgcgctgc attagctagt tggtaaggta acggcttacc aaggcaacga tacgtagccg 300  
 acctgagagg gtgatcggcc acactggaac tgagacacgg tccagactcc tacgggaggc 360  
 agcagtaggg aatcttccgc aatggggcga agcctgacgg agcaacgccg cgtgagtgat 420  
 gaaggtcttc ggatcgtaaa actctgttat tagggaagaa catatgtgta agtaactgtg 480  
 cacatcttga cggtaacctaa tcagaaagcc acggctaact acgtgccagc agccgcggta 540

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atacgtagggt ggcaagcggt atccggaatt attgggcgta aagcgcgcgt aggcgggtttt 600
ttaagtctga tgtgaaagcc cacgggtcaa cctggagggt tcattggaaa ctggaaaact 660
tgagtgcaga agaggaaagt ggaattccat gtgtagcgggt gaaatgcgca gagatatgga 720
ggaacaccag tggcgaaggc gactttcttg tctgtaactg acgctgatgt gcgaaagcgt 780
ggggatcaaa caggattaga taccctggta gtccacgccg taaacgatga gtgctaagt 840
ttagggggtt tccgccccct agtgctgcag ctaacgcatt aagcactccg cctggggagt 900
acgaccgcaa ggttgaaact caaaggaatt gacggggacc cgcacaagcg gtggagcatg 960
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gtgaatacgt tcccgggtat tgtacacacc gcccgtcaca ccacgagagt ttgtaacacc 1440
cgaagccggt ggagtaacct tttaggagct agccgtcgaa ggtgggacaa atgattgggg 1500
tgaagtcgta acaaggtagc cgtatcggaa ggtgcggctg gatcacctcc tttct 1555

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&lt;210&gt; 22

&lt;211&gt; 1294

&lt;212&gt; DNA

<213> *Staphylococcus aureus*

&lt;400&gt; 22

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aagatgactg aagaattcaa tgaatcaatg attaacgata ttaaagaagg tgacaaagtc 120
actggcgagg tacaacaagt tgaagacaag caagttgttg ttcatatcaa cgggtggtaaa 180
tttaatggga ttattccctat tagtcaacta tctacgcata atattgatag cccaagttaa 240
gttgtaaaag agggcgacga agttgaagca tatgtcacta aagttgagtt tgatgaagaa 300
aatgaaactg gagcttacat cttatctaga agacaacttg aaactgagaa gtcttatagt 360
tattttacaag aaaaattaga taataatgaa atcatcgaag cgaaagtaac agaagtagtt 420
aaagggtggt tgggtgttga tgtaggacaa agaggttttg ttccggcttc actaatttca 480
acagacttca ttgaggattt ctctgtgttt gatggacaaa caattcgtat taaagttgaa 540
gaattggatc ctgaaaataa tagagtcatt ttaagccgta aagcagttga acaagaagaa 600
aacgatgcta aaaaagatca attattacaa tctttaaatg aaggcgatgt tattgatggt 660
aaagtagcgc gtttaactca atttggtgca tttatagaca ttggcgggtg tgatggttta 720
gtgcatgtat ctgaactttc tcacgaacat gttcaaacac cagaagaagt agtttcaatt 780
ggtcaagatg ttaaagttaa aattaaatct attgatagag atacagaacg tatttcatta 840
tcaatcaaag atacgttacc aacacctttc gaaaatatta aaggtcaatt ccacgaaaat 900
gatgtcattg aagggtgtcg agtaagattg gcaaactttg gtgcatttgt tgaaattgca 960
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aatgaaagag taccactata tattaaagca acattaccaa acgaagatgt tgttgaaagt 1140
gatccttcta cgactaaggc gtacttagaa aacgaagaag aagataatcc aacaattggc 1200
gatatgattg gtgataaact taaaaatctt aaactataat ttaatattta atagtcaact 1260
ccacatgttt atgattgcat gtggagtatt tttta 1294

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&lt;210&gt; 23

&lt;211&gt; 391

&lt;212&gt; PRT

<213> *Staphylococcus aureus*

&lt;400&gt; 23

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Met Thr Glu Glu Phe Asn Glu Ser Met Ile Asn Asp Ile Lys Glu Gly
  1           5           10           15

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Asp Lys Val Thr Gly Glu Val Gln Gln Val Glu Asp Lys Gln Val Val
      20           25           30

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Val His Ile Asn Gly Gly Lys Phe Asn Gly Ile Ile Pro Ile Ser Gln

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35					40					45					
Leu	Ser	Thr	His	His	Ile	Asp	Ser	Pro	Ser	Glu	Val	Val	Lys	Glu	Gly
50						55					60				
Asp	Glu	Val	Glu	Ala	Tyr	Val	Thr	Lys	Val	Glu	Phe	Asp	Glu	Glu	Asn
65					70					75					80
Glu	Thr	Gly	Ala	Tyr	Ile	Leu	Ser	Arg	Arg	Gln	Leu	Glu	Thr	Glu	Lys
				85					90					95	
Ser	Tyr	Ser	Tyr	Leu	Gln	Glu	Lys	Leu	Asp	Asn	Asn	Glu	Ile	Ile	Glu
			100					105					110		
Ala	Lys	Val	Thr	Glu	Val	Val	Lys	Gly	Gly	Leu	Val	Val	Asp	Val	Gly
		115						120					125		
Gln	Arg	Gly	Phe	Val	Pro	Ala	Ser	Leu	Ile	Ser	Thr	Asp	Phe	Ile	Glu
	130					135					140				
Asp	Phe	Ser	Val	Phe	Asp	Gly	Gln	Thr	Ile	Arg	Ile	Lys	Val	Glu	Glu
145					150					155					160
Leu	Asp	Pro	Glu	Asn	Asn	Arg	Val	Ile	Leu	Ser	Arg	Lys	Ala	Val	Glu
				165					170					175	
Gln	Glu	Glu	Asn	Asp	Ala	Lys	Lys	Asp	Gln	Leu	Leu	Gln	Ser	Leu	Asn
			180					185					190		
Glu	Gly	Asp	Val	Ile	Asp	Gly	Lys	Val	Ala	Arg	Leu	Thr	Gln	Phe	Gly
	195						200					205			
Ala	Phe	Ile	Asp	Ile	Gly	Gly	Val	Asp	Gly	Leu	Val	His	Val	Ser	Glu
	210					215					220				
Leu	Ser	His	Glu	His	Val	Gln	Thr	Pro	Glu	Glu	Val	Val	Ser	Ile	Gly
225					230					235					240
Gln	Asp	Val	Lys	Val	Lys	Ile	Lys	Ser	Ile	Asp	Arg	Asp	Thr	Glu	Arg
			245						250					255	
Ile	Ser	Leu	Ser	Ile	Lys	Asp	Thr	Leu	Pro	Thr	Pro	Phe	Glu	Asn	Ile
		260						265					270		
Lys	Gly	Gln	Phe	His	Glu	Asn	Asp	Val	Ile	Glu	Gly	Val	Val	Val	Arg
	275						280					285			
Leu	Ala	Asn	Phe	Gly	Ala	Phe	Val	Glu	Ile	Ala	Pro	Gly	Val	Gln	Gly
	290					295					300				
Leu	Val	His	Ile	Ser	Glu	Ile	Ala	His	Lys	His	Ile	Gly	Thr	Pro	Gly
305					310					315					320
Glu	Val	Leu	Glu	Pro	Gly	Gln	Gln	Val	Asn	Val	Lys	Ile	Leu	Gly	Ile
				325					330					335	
Asp	Glu	Glu	Asn	Glu	Arg	Val	Ser	Leu	Ser	Ile	Lys	Ala	Thr	Leu	Pro
			340					345					350		
Asn	Glu	Asp	Val	Val	Glu	Ser	Asp	Pro	Ser	Thr	Thr	Lys	Ala	Tyr	Leu
	355						360					365			

Glu Asn Glu Glu Glu Asp Asn Pro Thr Ile Gly Asp Met Ile Gly Asp  
 370 375 380

Lys Leu Lys Asn Leu Lys Leu  
 385 390

<210> 24  
 <211> 924  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 24  
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 cggttggaacc caaaaatgaa aaaatatatc ttactgaga gaaatggtat ttatatcatc 180  
 gacttacaaa aaacagtga aaaagtagac gaggcataca acttcttgaa acaagtttca 240  
 gaagatggtg gacaagtctt attcgttaga nctaaaaaac aagcacaaga atcagtttaa 300  
 tctgaagcag aacgtgctgg tcaattctac attaaccaaa gatggttagg tggattatta 360  
 actaactata aaacgatctc aaaacgaatc aaacgtattt ctgaaattga aaaaatggaa 420  
 gaagatggtt tattcgaagt attacctaaa aaagaagtag tagaacttaa aaaagaatac 480  
 gaccgtttta tcaaattctt aggcggaatt cgtgatatga aatcaatgcc tcaagcatta 540  
 ttcgtagttg acccacgtaa agagcgtaat gcaattgctg aagctcgtaa attaaatatt 600  
 cctatcgtag gtatcggtga cactaactgt gatcctgacg aaattgacta cgttatccca 660  
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 ttagaagggtc aacaaggcgt ttctaataaa gaagtagctg cagaacaaaa catcgattta 780  
 gatgaaaaag aaaaatcaga agaaacagaa gcaactgaag aataatcaac tgttgaatct 840  
 gacttagata tagtttaa at gggtgataag atattaatgc ttatcacctt ttttaaaaag 900  
 aaaatcgagg caaattacaa atat 924

<210> 25  
 <211> 255  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 25  
 Met Ala Val Ile Ser Met Lys Gln Leu Leu Glu Ala Gly Val Xaa Phe  
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 Gly His Gln Thr Arg Arg Trp Asn Pro Lys Met Lys Lys Tyr Ile Phe  
 20 25 30  
 Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Lys Thr Val Lys  
 35 40 45  
 Lys Val Asp Glu Ala Tyr Asn Phe Leu Lys Gln Val Ser Glu Asp Gly  
 50 55 60  
 Gly Gln Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Val  
 65 70 75 80  
 Lys Ser Glu Ala Glu Arg Ala Gly Gln Phe Tyr Ile Asn Gln Arg Trp  
 85 90 95  
 Leu Gly Gly Leu Leu Thr Asn Tyr Lys Thr Ile Ser Lys Arg Ile Lys  
 100 105 110  
 Arg Ile Ser Glu Ile Glu Lys Met Glu Glu Asp Gly Leu Phe Glu Val  
 115 120 125  
 Leu Pro Lys Lys Glu Val Val Glu Leu Lys Lys Glu Tyr Asp Arg Leu

130	135	140
Ile Lys Phe Leu Gly Gly Ile Arg Asp Met Lys Ser Met Pro Gln Ala		
145	150	155 160
Leu Phe Val Val Asp Pro Arg Lys Glu Arg Asn Ala Ile Ala Glu Ala		
	165	170 175
Arg Lys Leu Asn Ile Pro Ile Val Gly Ile Val Asp Thr Asn Cys Asp		
	180	185 190
Pro Asp Glu Ile Asp Tyr Val Ile Pro Ala Asn Asp Asp Ala Ile Arg		
	195	200 205
Ala Val Lys Leu Leu Thr Ala Lys Met Ala Asp Ala Ile Leu Glu Gly		
	210	215 220
Gln Gln Gly Val Ser Asn Glu Glu Val Ala Ala Glu Gln Asn Ile Asp		
	225	230 235 240
Leu Asp Glu Lys Glu Lys Ser Glu Glu Thr Glu Ala Thr Glu Glu		
	245	250 255

<210> 26  
 <211> 800  
 <212> DNA  
 <213> Staphylococcus aureus

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 gtgttggtat tatccgtgat tgggaagcta aatgggtatgc tgaaaaagac ttcgcttcac 180  
 ttttacacga agatttaaaa atccgtaaat ttattgataa tgaattaaaa gaagcatcag 240  
 tttctcacgt agagattgaa cgtgctgcaa accgtatcaa cattgcaatt catactggta 300  
 aacctgggtat ggtaattgggt aaaggcgggt cagaaatcga aaaattacgc aacaaattaa 360  
 atgcgttaac tgataaaaaa gtacacatca acgtaattga aatcaaaaaa gttgatcttg 420  
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 acatcgtcct aaaacaactg 800

<210> 27  
 <211> 221  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 27  
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 20 25 30  
 Ala Ser Leu Leu His Glu Asp Leu Lys Ile Arg Lys Phe Ile Asp Asn  
 35 40 45  
 Glu Leu Lys Glu Ala Ser Val Ser His Val Glu Ile Glu Arg Ala Ala

50                                      55                                      60  
 Asn Arg Ile Asn Ile Ala Ile His Thr Gly Lys Pro Gly Met Val Ile  
 65                                      70                                      75                                      80  
 Gly Lys Gly Gly Ser Glu Ile Glu Lys Leu Arg Asn Lys Leu Asn Ala  
 85                                      90                                      95  
 Leu Thr Asp Lys Lys Val His Ile Asn Val Ile Glu Ile Lys Lys Val  
 100                                      105                                      110  
 Asp Leu Asp Ala Arg Leu Val Ala Glu Asn Ile Ala Arg Gln Leu Glu  
 115                                      120                                      125  
 Asn Arg Ala Ser Phe Arg Arg Val Gln Lys Gln Ala Ile Thr Arg Ala  
 130                                      135                                      140  
 Met Lys Leu Gly Ala Lys Gly Ile Lys Thr Gln Val Ser Gly Arg Leu  
 145                                      150                                      155                                      160  
 Gly Gly Ala Asp Ile Ala Arg Ala Glu Gln Tyr Ser Glu Gly Thr Val  
 165                                      170                                      175  
 Pro Leu His Thr Leu Arg Ala Asp Ile Asp Tyr Ala His Ala Glu Ala  
 180                                      185                                      190  
 Asp Thr Thr Tyr Gly Lys Leu Gly Val Lys Val Trp Ile Tyr Arg Gly  
 195                                      200                                      205  
 Glu Val Leu Pro Thr Lys Asn Thr Ser Gly Gly Gly Lys  
 210                                      215                                      220

&lt;210&gt; 28

&lt;211&gt; 639

&lt;212&gt; DNA

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 28

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 gaggtaccag aagcaatcaa aaaagctggt gaagcagcta aaaaagattt agtagttgtt 300  
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 aaattacgtg gcaaaacagt agaagaatta tacaattaag gagggaaaac tagttatggc 600  
 taaattacaa attaccctca ctcgtagtgt tattggtcg 639

&lt;210&gt; 29

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 29

Met Ala Arg Arg Glu Glu Thr Lys Glu Phe Glu Glu Arg Val Val  
 1                                      5                                      10                                      15  
 Thr Ile Asn Arg Val Ala Lys Val Val Lys Gly Gly Arg Arg Phe Arg



	20		25		30
Phe Thr Ala Leu Val Val Val Gly Asp Lys Asn Gly Arg Val Gly Phe	35	40	45		
Gly Thr Gly Lys Ala Gln Glu Val Pro Glu Ala Ile Lys Lys Ala Val	50	55	60		
Glu Ala Ala Lys Lys Asp Leu Val Val Val Pro Arg Val Glu Gly Thr	65	70	75	80	
Thr Pro His Thr Ile Thr Gly Arg Tyr Gly Ser Gly Ser Val Phe Met	85	90		95	
Lys Pro Ala Ala Pro Gly Thr Gly Val Ile Ala Gly Gly Pro Val Arg	100	105	110		
Ala Val Leu Glu Leu Ala Gly Ile Thr Asp Ile Leu Ser Lys Ser Leu	115	120	125		
Gly Ser Asn Thr Pro Ile Asn Met Val Arg Ala Thr Ile Asp Gly Leu	130	135	140		
Gln Asn Leu Lys Asn Ala Glu Asp Val Ala Lys Leu Arg Gly Lys Thr	145	150	155	160	
Val Glu Glu Leu Tyr Asn	165				

<210> 30  
 <211> 499  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 30  
 gcgcacatgata taattcttta ttgtgagtaa tgaaaattat tccttgctta tctgttttaa 60  
 gattgataag ccgtatagac cacaaggagg tgcaaatata aaatgagaac atatgaagtt 120  
 atgtacatcg tacgcccata cattgaggaa gatgctaaaa aagcgtagt tgaacgtttc 180  
 aacggatatc tagctactga aggtgcagaa gttttagaag caaaagactg gggtaaactg 240  
 cgccatagctt atgaaatcaa tgatttcaaa gatggcttct acaacatcgt acgtgttaaa 300  
 tctgataaca acaaagctac tgacgaattc caacgtctag ctaaaatcag tgacgatatc 360  
 attcggtaca tgggtattcg tgaagacgaa gacaagtaat aattagaggg ggcgttttaa 420  
 tgctaaatag agttgtatta gtaggctcgt taacgaaaga tccggaatac agaaccactc 480  
 cctcaggtgt gactgtagc 499

<210> 31  
 <211> 98  
 <212> PRT  
 <213> Staphylococcus aureus

Met Arg Thr Tyr Glu Val Met Tyr Ile Val Arg Pro Asn Ile Glu Glu	1	5	10	15
Asp Ala Lys Lys Ala Leu Val Glu Arg Phe Asn Gly Ile Leu Ala Thr	20	25	30	
Glu Gly Ala Glu Val Leu Glu Ala Lys Asp Trp Gly Lys Arg Arg Leu	35	40	45	

Ala Tyr Glu Ile Asn Asp Phe Lys Asp Gly Phe Tyr Asn Ile Val Arg  
 50 55 60

Val Lys Ser Asp Asn Asn Lys Ala Thr Asp Glu Phe Gln Arg Leu Ala  
 65 70 75 80

Lys Ile Ser Asp Asp Ile Ile Arg Tyr Met Val Ile Arg Glu Asp Glu  
 85 90 95

Asp Lys

<210> 32  
 <211> 462  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 32  
 gtgcacaaca accagaaaac tacgaattac gtgggttaatt agaaggagga aatgactttg 60  
 gcacaagttg aatatagagg cacaggccgt cgtaaaaact cagtagcacg tgtacgttta 120  
 gtaccagggtg aaggtaacat cacagttaat aaccgtgacg tacgcgaata cttaccattc 180  
 gaatcattaa ttttagactt aaaccaacca tttgatgtaa ctgaaactaa aggtaactat 240  
 gatgttttag ttaacgttca tgggtggtggt ttcactggac aagctcaagc tatccgtcac 300  
 ggaatcgctc gtgcattatt agaagcagat cctgaataca gaggttcttt aaaacgcgct 360  
 ggattactta ctcgtagacc acgtatgaaa gaacgtaaaa aaccagggtct taaagcagct 420  
 cgctcggtcac ctcaattctc aaaacgttaa ttgtcggacg at 462

<210> 33  
 <211> 132  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 33  
 Met Thr Leu Ala Gln Val Glu Tyr Arg Gly Thr Gly Arg Arg Lys Asn  
 1 5 10 15

Ser Val Ala Arg Val Arg Leu Val Pro Gly Glu Gly Asn Ile Thr Val  
 20 25 30

Asn Asn Arg Asp Val Arg Glu Tyr Leu Pro Phe Glu Ser Leu Ile Leu  
 35 40 45

Asp Leu Asn Gln Pro Phe Asp Val Thr Glu Thr Lys Gly Asn Tyr Asp  
 50 55 60

Val Leu Val Asn Val His Gly Gly Gly Phe Thr Gly Gln Ala Gln Ala  
 65 70 75 80

Ile Arg His Gly Ile Ala Arg Ala Leu Leu Glu Ala Asp Pro Glu Tyr  
 85 90 95

Arg Gly Ser Leu Lys Arg Ala Gly Leu Leu Thr Arg Asp Pro Arg Met  
 100 105 110

Lys Glu Arg Lys Lys Pro Gly Leu Lys Ala Ala Arg Arg Ser Pro Gln  
 115 120 125

Phe Ser Lys Arg  
 130

<210> 34  
 <211> 441  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 34  
 aggttactga cacacccggc cgctttgcca tggcgcgtgtg taagatagtt ttcgtggaga 60  
 agtctatcac taaatgtaga cgaataagga gggaaaatta tggcaaaaca aaaaatcaga 120  
 atcagattaa aagcttatga tcaccgcgta attgatcaat cagcagagaa gattgtagaa 180  
 acagcgaaac gttctgggtgc agatgtttct ggaccaattc cgttaccaac tgagaaatca 240  
 cgtacacaca aacgtttaat cgatattgta aaccaaacac caaaaacagt tgacgcttta 300  
 atgggcttaa acttaccatc tgggtgtagac atcgaaatca aattataata gacaatttta 360  
 ggaggtggac tttcgtatgac caaaggaatc ttaggaagaa aaattgggat gacacaagta 420  
 ttcggagaaa acggtgaatt a 441

<210> 35  
 <211> 102  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 35  
 Met Ala Lys Gln Lys Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Arg  
 1 5 10 15  
 Val Ile Asp Gln Ser Ala Glu Lys Ile Val Glu Thr Ala Lys Arg Ser  
 20 25 30  
 Gly Ala Asp Val Ser Gly Pro Ile Pro Leu Pro Thr Glu Lys Ser Val  
 35 40 45  
 Tyr Thr Ile Ile Arg Ala Val His Lys Tyr Lys Asp Ser Arg Glu Gln  
 50 55 60  
 Phe Glu Gln Arg Thr His Lys Arg Leu Ile Asp Ile Val Asn Pro Thr  
 65 70 75 80  
 Pro Lys Thr Val Asp Ala Leu Met Gly Leu Asn Leu Pro Ser Gly Val  
 85 90 95  
 Asp Ile Glu Ile Lys Leu  
 100

<210> 36  
 <211> 594  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 36  
 agttcgtggt caaaaaacga aaaacmacgc gcgtactcgt aaaggaccag ttaaaacggg 60  
 agctaacaag aaaaatmat aggtaaagga ggcaaatttt aaatggcacg taaacaagta 120  
 tctcgtaaac gtagagtga aaagaatatt gaaaatgggtg tagcacacat ccgttcaaca 180  
 ttcaacaaca ctattgtaac tatcactgat gagttcggta atgctttatc atgggtcatca 240  
 gctgggtgcat taggattcaa aggatctaaa aaatcaaacac catttgcagc acaaatggct 300  
 tctgaaactg catctaaatc agctatggag catgggttaa aaacagttga agtaacagtt 360  
 aaaggacctg gtccagggtcg tgaatcagct attcgtgcat tacaatctgc aggtttagaa 420  
 gtaactgcga tcagagacgt tactccagta cctcataacg gttgtcgtcc accaaaacgt 480  
 cgtcgtgtat aatttatgat ggtattgtta caggctcactg agcaaacatt ttaaattaag 540  
 tcgacgtata taaggaggat atttaaatga tagaaatcga aaaacctaga attg 594

```
<400> 39
Met Pro Thr Ile Asn Gln Leu Val Arg Lys Pro Arg Gln Ser Lys Ile
   1                   5           10          15
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Lys Lys Ser Asp Ser Pro Ala Leu Asn Lys Gly Phe Asn Ser Lys Lys  
                   20                                  25                                  30  
 Lys Lys Phe Thr Asp Leu Asn Ser Pro Gln Lys Arg Gly Val Cys Thr  
                   35                                  40                                  45  
 Arg Val Gly Thr Met Thr Pro Lys Lys Pro Asn Ser Ala Leu Arg Lys  
                   50                                  55                                  60  
 Tyr Ala Arg Val Arg Leu Ser Asn Asn Ile Glu Ile Asn Ala Tyr Ile  
                   65                                  70                                  75                                  80  
 Pro Gly Ile Gly His Asn Leu Gln Glu His Ser Val Val Leu Val Arg  
                                   85                                  90                                  95  
 Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His Ile Val Arg  
                                   100                                  105                                  110  
 Gly Ala Leu Asp Thr Ser Gly Val Asp Gly Arg Arg Gln Gly Arg Ser  
                   115                                  120                                  125  
 Leu Tyr Gly Thr Lys Lys Pro Lys Asn  
                   130                                  135

<210> 40  
 <211> 633  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 40  
 gtataaaat gaaagtaaga ccatcagtaa aacctatttg cgaaaaatgt aaagtcatta 60  
 aacgtaaagg taaagtaatg gtaatttgtg aaaatccaaa acacaaacaa agacaagggt 120  
 aataaaagag aggtgtaaat taatatggca cgtattgcag gagtagatat tccacgtgaa 180  
 aaacgcgtag ttatctcatt aacttatata tacgggtatcg gtacgtcaac tgctcaaaaa 240  
 attcttgaag aagctaacgt atcagctgat actcgtgtga aagatttaac tgatgacgaa 300  
 ttaggtcgca tccgtgaagt tgtagacggt tataaagtcg aaggtgactt acgtcgtgaa 360  
 actaacttaa atatcaaacg tttaatggaa atttcatcat accgtgggtat ccgtcaccgt 420  
 cgtggtttac cagttcgtgg tcaaaaaaacg aaaaacaacg cgcgtactcg taaaggacca 480  
 gttaaaacgg tagctaacaa gaaaaataa taggtaaagg aggcaaattt taaatggcac 540  
 gtaaacaaagt atctcgtaaa cgtagagtga aaaagaatat tgaaaatggt gtagcacaca 600  
 tccgttcaac attcaacaac actattgtaa cta 633

<210> 41  
 <211> 121  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 41  
 Met Ala Arg Ile Ala Gly Val Asp Ile Pro Arg Glu Lys Arg Val Val  
                   1                                  5                                  10                                  15  
 Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Thr Ser Thr Ala Gln Lys  
                   20                                  25                                  30  
 Ile Leu Glu Glu Ala Asn Val Ser Ala Asp Thr Arg Val Lys Asp Leu  
                   35                                  40                                  45  
 Thr Asp Asp Glu Leu Gly Arg Ile Arg Glu Val Val Asp Gly Tyr Lys  
                   50                                  55                                  60

Val Glu Gly Asp Leu Arg Arg Glu Thr Asn Leu Asn Ile Lys Arg Leu  
65 70 75 80

Met Glu Ile Ser Ser Tyr Arg Gly Ile Arg His Arg Arg Gly Leu Pro  
85 90 95

Val Arg Gly Gln Lys Thr Lys Asn Asn Ala Arg Thr Arg Lys Gly Pro  
100 105 110

Val Lys Thr Val Ala Asn Lys Lys Lys  
115 120

<210> 42

<211> 311

<212> DNA

<213> Staphylococcus aureus

<400> 42

ctcgtgaatt gttagctaac ttcggtatgc cattccgtaa ataattatTT aaaggaggct 60  
aattaagtgg ctaaaacttc aatgggttgct aagcaacaaa aaaaacaaaa atatgcagtt 120  
cgtgaataca ctcgttgtga acgttgtggc cgtccacatt ctgtatatcg taaattttaa 180  
ttatgccgta tttgtttccg tgaattagct tacaaaggcc aaatccctgg cgttcgtaaa 240  
gctagctggg aataaaaaag agtctgaaag gaggcaacaa tcaatgacaa tgacagatcc 300  
aatcgcatg a 311

<210> 43

<211> 61

<212> PRT

<213> Staphylococcus aureus

<400> 43

Met Ala Lys Thr Ser Met Val Ala Lys Gln Gln Lys Lys Gln Lys Tyr  
1 5 10 15

Ala Val Arg Glu Tyr Thr Arg Cys Glu Arg Cys Gly Arg Pro His Ser  
20 25 30

Val Tyr Arg Lys Phe Lys Leu Cys Arg Ile Cys Phe Arg Glu Leu Ala  
35 40 45

Tyr Lys Gly Gln Ile Pro Gly Val Arg Lys Ala Ser Trp  
50 55 60

<210> 44

<211> 710

<212> DNA

<213> Staphylococcus aureus

<400> 44

aacattcata cacctgttaa tattatttct ttagaaaaat aaaaattaaa acatgactta 60  
aaggagattt tataaatggc agttaaaatt cgtttaaacac gtttaggttc aaaaagaaat 120  
ccattctatc gtatcgtagt agcagatgct cgttctccac gtgacggacg tatcatcgaa 180  
caaatcggtta cttataaccc aacgagcgct aatgctccag aaattaaagt tgacgaagcg 240  
ttagcttttaa aatgggttaa tgatgggtgc aaaccaactg atacagttca caatatctta 300  
tcaaaagaag gtattatgaa aaaatttgac gaacaaaaga aagctaagta atttagcgta 360  
aaattgttct aacaataaga ataactcgtt tacactgaca gttattactc aatgatacgt 420  
tggaatatat acatgttagt aatatagaac gtttgggtac cataatgggtg ccctttttct 480  
ttgaattatt ttcaattaaa atagaagtgg tcaaaagcata gagttggagg taatagaatg 540

agagttgaag ttggtcaaaa ttgtttacac acacgggggtt taaaagggtgg aaattaaagg 600  
 taaatccatt tcagaccttt tacagaccgg ttcggttttc aaccccggtc caaagatgcc 660  
 tgaccagttg ggccttaaac caaattaaac cgacccctt ggaaatatta 710

<210> 45  
 <211> 92  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 45  
 Met Ala Val Lys Ile Arg Leu Thr Arg Leu Gly Ser Lys Arg Asn Pro  
 1 5 10 15  
 Phe Tyr Arg Ile Ile Val Val Ala Asp Ala Arg Ser Pro Arg Asp Gly  
 20 25 30  
 Arg Ile Ile Glu Gln Ile Gly Thr Tyr Asn Pro Thr Ser Ala Asn Ala  
 35 40 45  
 Pro Glu Ile Lys Val Asp Glu Ala Leu Ala Leu Lys Trp Leu Asn Asp  
 50 55 60  
 Gly Ala Lys Pro Thr Asp Thr Val His Asn Ile Leu Ser Lys Glu Gly  
 65 70 75 80  
 Ile Met Lys Lys Phe Asp Glu Gln Lys Lys Ala Lys  
 85 90

<210> 46  
 <211> 437  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 46  
 aatgcaaacg gaccgattga tataagtgat gatgacttac cattctaata aaaattaacg 60  
 aaattaaagc gaaaaaatta tcaaaggagg cacacaatca tggcaggtgg accaagaaga 120  
 ggcggacgtc gtcgtaaaaa agtatgctat ttcacagcaa atggtattac acatatcgac 180  
 tacaaagaca ctgaattatt aaaacgtttt atctcagaac gcggtaaaat tttaccacgt 240  
 cgtgttaactg gtacttcagc taaatatcaa cgtatgttga ctacagctat caaacgttct 300  
 cgtcatatgg cattattacc atatgttaaa gaagaacaat aatatataat ttattgtcaa 360  
 accccgtagg cataggctta cggggccttt tgtgttttgg ggtatagaaa aaggggcaaaa 420  
 aggatgatgt gaatgtt 437

<210> 47  
 <211> 80  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 47  
 Met Ala Gly Gly Pro Arg Arg Gly Gly Arg Arg Arg Lys Lys Val Cys  
 1 5 10 15  
 Tyr Phe Thr Ala Asn Gly Ile Thr His Ile Asp Tyr Lys Asp Thr Glu  
 20 25 30  
 Leu Leu Lys Arg Phe Ile Ser Glu Arg Gly Lys Ile Leu Pro Arg Arg  
 35 40 45  
 Val Thr Gly Thr Ser Ala Lys Tyr Gln Arg Met Leu Thr Thr Ala Ile

50 55 60  
 Lys Arg Ser Arg His Met Ala Leu Leu Pro Tyr Val Lys Glu Glu Gln  
 65 70 75 80

<210> 48  
 <211> 478  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 48  
 aaacttatcg ttcgtggacg taagaaaaaa taatataatc aacttatttg ggtgtgcggc 60  
 ttaaagctgc acgcacataa taagaaggga ggcgcccaaa tggctcgtag tattaataaaa 120  
 ggacctttcg tcgatgagca tttaatgaaa aaagttgaag ctcaagaagg aagcgaaaag 180  
 aaacaagtaa tcaaaacatg gtcacgtcgt tctacaattt tccctaattt catcggacat 240  
 acttttgcag tatacgacgg acgtaaacac gtacctgtat atgtaactga agatatggta 300  
 ggtcataaat taggtgagtt tgctcctact cgtacattca aaggacacgt tgcagacgac 360  
 aagaaaacaa gaagataata tctattaagt agaggaggac atcctaattg aagcaaaagc 420  
 ggttgctaga acaataagaa tcgcacctcg taaagtaaga ctagttcttg acttaatc 478

<210> 49  
 <211> 92  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 49  
 Met Ala Arg Ser Ile Lys Lys Gly Pro Phe Val Asp Glu His Leu Met  
 1 5 10 15  
 Lys Lys Val Glu Ala Gln Glu Gly Ser Glu Lys Lys Gln Val Ile Lys  
 20 25 30  
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Phe Ile Gly His Thr  
 35 40 45  
 Phe Ala Val Tyr Asp Gly Arg Lys His Val Pro Val Tyr Val Thr Glu  
 50 55 60  
 Asp Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Phe  
 65 70 75 80  
 Lys Gly His Val Ala Asp Asp Lys Lys Thr Arg Arg  
 85 90

<210> 50  
 <211> 520  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 50  
 tgcaaaattt taagctaacc ccatcaaata aatgattgca caacggttag actttttgta 60  
 aaatatttct tgttgtaatc aaataaaaatt ttgataagat gaactcactt ttaggaggtg 120  
 gcagaaatgg caaatatcaa atctgcaatt aaacgtgtaa aaacaactga aaaagctgaa 180  
 gcacgcaaca tttcacaaaa gagtgcaatg cgtacagcag ttaaaaaacgc taaaacagct 240  
 gtttcaaata acgctgataa taaaaatgaa ttagtaagct tagcagttaa gttagtagac 300  
 aaagctgctc aaagtaattt aatacattca aacaaagctg accgtattaa atcacaaata 360



atgactgcaa ataaataatc tttttaaata aaagttcaag cgcattgcttg aactttttatt 420  
 ttttataaag atagaatgaa taattccagt attaactgtt tatccatata tgatgattta 480  
 agttttataat cagttttccgc acaagcatct ataattattca 520

<210> 51  
 <211> 499  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 51  
 tgttttcaaat aaaaaacaat ttactaattg accataaatt acagatatat tatactttata 60  
 aatgcatagt ttactgtgc aattgactat aaagttccgt tgatatttgg agggaggggaa 120  
 atacagatgt ctaaaacagt agtacgtaaa aatgaatcac ttgaagatgc gttacgtaga 180  
 tttaaacggt cagttttctaa aagtggaaaca atccaagaag tacgtaaacg tgaattttac 240  
 gaaaaaccaa gcgtaaaacg taaaaagaaa tcagaagctg cacgtaaacg taaattcaaa 300  
 taattaatac ctctgttgac tccctcaaca cgaatattaa ttatataaaa caaacatcac 360  
 aagtttagtgt ctgacactaa tatgtgatgt tttttgttg tcaattttta attaaaaaaa 420  
 gttatatagt ttataaataa tcaattgat attctatagg ttcttataac tataaagtat 480  
 attcaatttc atgtataat 499

<210> 52  
 <211> 58  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 52  
 Met Ser Lys Thr Val Val Arg Lys Asn Glu Ser Leu Glu Asp Ala Leu  
 1 5 10 15  
 Arg Arg Phe Lys Arg Ser Val Ser Lys Ser Gly Thr Ile Gln Glu Val  
 20 25 30  
 Arg Lys Arg Glu Phe Tyr Glu Lys Pro Ser Val Lys Arg Lys Lys Lys  
 35 40 45  
 Ser Glu Ala Ala Arg Lys Arg Lys Phe Lys  
 50 55

<210> 53  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR Primer

<400> 53  
 tatattatcg ataatggctc gattcagagg t 31

<210> 54  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR Primer

<400> 54

tataggatcc ttaacggatt aattgttcgt taattt 36

<210> 55  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 55  
tatattatcg ataatggcag gtggaccaag aag 33

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 56  
tataggatcc ttattgttct tctttaacat 30

<210> 57  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 57  
tatattatcg ataatgaaga aacatatgaa gttat 35

<210> 58  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 58  
tataggatcc ttacttgtct tcgtcttcac 30

<210> 59  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 59  
caccacgaga gtttgtaac

<210> 60  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 60  
caccccaatc atttgtccac

<210> 61  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 61  
cacgtggata acctaccta

<210> 62  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR Primer

<400> 62  
gtggccgata accctctcagg